

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 20, 2003, 13:23:03 ; Search time 15.2099 Seconds  
(without alignments)  
489.597 Million cell updates/sec

Title: US-09-855-266A-1  
Perfect score: 1000  
Sequence: 1 MVTFSHYSSLHSHWFLLLLLL.....SSVSNPRNWLFLMLIVFCI 176

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2.6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2.6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2.6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2.6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2.6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1000	100.0	176	US-09-411-722-1	Sequence 1, Appl1
2	858	85.8	148	US-09-411-722-2	Sequence 2, Appl1
3	206.5	20.6	355	US-08-292-549-6	Sequence 6, Appl1
4	206.5	20.6	355	US-09-006-353A-14	Sequence 14, Appl1
5	206.5	20.6	355	US-09-573-986-14	Sequence 14, Appl1
6	205.5	20.5	167	US-08-050-319B-2	Sequence 2, Appl1
7	205.5	20.5	167	US-08-050-319B-57	Sequence 57, Appl1
8	205.5	20.5	167	US-08-465-982-2	Sequence 2, Appl1
9	205.5	20.5	167	US-08-465-982-57	Sequence 57, Appl1
10	205.5	20.5	197	US-08-828-683A-21	Sequence 21, Appl1
11	205.5	20.5	280	US-08-974-022-46	Sequence 46, Appl1
12	205.5	20.5	280	US-08-795-445A-46	Sequence 46, Appl1
13	205.5	20.5	280	US-08-795-447A-46	Sequence 46, Appl1
14	205.5	20.5	280	US-08-974-186-46	Sequence 46, Appl1
15	205.5	20.5	280	US-08-795-446B-46	Sequence 46, Appl1
16	205.5	20.5	280	US-08-706-945D-132	Sequence 132, App
17	205.5	20.5	455	US-08-050-319B-25	Sequence 25, Appl1
18	205.5	20.5	455	US-08-321-668-2	Sequence 2, Appl1
19	205.5	20.5	455	US-08-837-941-2	Sequence 2, Appl1
20	205.5	20.5	455	US-08-126-016-2	Sequence 2, Appl1
21	205.5	20.5	455	US-08-465-982-25	Sequence 25, Appl1
22	205.5	20.5	455	US-08-815-469-5	Sequence 5, Appl1
23	205.5	20.5	455	US-09-006-353A-3	Sequence 3, Appl1
24	205.5	20.5	455	US-09-527-236A-5	Sequence 5, Appl1
25	205.5	20.5	455	US-08-054-970-2	Sequence 2, Appl1
26	205.5	20.5	455	US-09-565-918-4	Sequence 4, Appl1
27	205.5	20.5	455	US-09-573-986-3	Sequence 3, Appl1

28	205.5	20.5	455	4	US-09-027-287-3	Sequence 3, Appl1
29	205.5	20.5	455	4	US-09-252-656B-3	Sequence 3, Appl1
30	205.5	20.5	455	4	US-08-406-824A-4	Sequence 4, Appl1
31	205	20.5	327	3	US-09-290-640-66	Sequence 66, Appl1
32	204.5	20.4	199	1	US-08-050-319B-48	Sequence 48, Appl1
33	204.5	20.4	199	2	US-08-465-982-48	Sequence 48, Appl1
34	204.5	20.4	285	3	US-08-804-166-6	Sequence 6, Appl1
35	204.5	20.4	285	3	US-08-910-991-6	Sequence 6, Appl1
36	202.5	20.2	349	3	US-09-006-353A-13	Sequence 13, Appl1
37	202.5	20.2	349	4	US-09-573-986-13	Sequence 13, Appl1
38	200.5	20.1	139	4	US-08-706-945D-129	Sequence 129, App
39	200.5	20.1	153	2	US-08-219-237B-4	Sequence 4, Appl1
40	200.5	20.1	153	3	US-08-477-347-12	Sequence 12, Appl1
41	200.5	20.1	153	3	US-08-476-862-3	Sequence 3, Appl1
42	200.5	20.1	153	3	US-08-468-560C-4	Sequence 4, Appl1
43	200.5	20.1	153	4	US-09-800-909-3	Sequence 3, Appl1
44	200.5	20.1	154	4	US-08-828-683A-12	Sequence 12, Appl1
45	200.5	20.1	161	4	US-09-326-394A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1  
US-09-411-722-1  
; Sequence 1, Application US/09411722  
; Patent No. 6271366  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501/040001  
; CURRENT APPLICATION NUMBER: US/09/411,722  
; CURRENT FILING DATE: 1999-10-01  
; PRIOR FILING DATE: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-411-722-1

Query Match	100.0%	Score 1000;	DB 3;	Length 176;
Best Local Similarity	100.0%	Pred. No. 2.7e-85;		
Matches	176;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	MVTFSHYSSLHSHWFLLLLLLNLFLPVIFAMPESYSFNC	PDGEYQSDVCCKTCPSGTFVK	60
Db	1	MVTFSHYSSLHSHWFLLLLLLNLFLPVIFAMPESYSFNC	PDGEYQSDVCCKTCPSGTFVK	60
QY	61	APCKIPHTQGCCKCHPTFTGKDNGLHDCSTCDKQDNWADCSATS	DRKCECQIGL	120
Db	61	APCKIPHTQGCCKCHPTFTGKDNGLHDCSTCDKQDNWADCSATS	DRKCECQIGL	120
QY	121	YYDPKPFESCRPCTKCPQIGIPVLQECNSTANTVCCSSSVSNPRNWL	FLMLIVFCI	176
Db	121	YYDPKPFESCRPCTKCPQIGIPVLQECNSTANTVCCSSSVSNPRNWL	FLMLIVFCI	176

RESULT 2  
US-09-411-722-2  
; Sequence 2, Application US/09411722  
; Patent No. 6271366  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501/040001  
; CURRENT APPLICATION NUMBER: US/09/411,722

;; CURRENT FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: JP 9/099653  
;; PRIOR FILING DATE: 1997-04-01  
;; NUMBER OF SEQ ID NOS: 12  
;; SOFTWARE: FastSeq for Windows version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 148  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-411-722-2

Query Match 85.8%; Score 958; DB 3; Length 148;  
Best Local Similarity 100.0%; Pred. No. 3e-72;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 AMPESYFNCPDGEYQSNVDCCKTCPSGTFVKAPCKIPHTOGQCEKCHPGFTGKDNGLH 88  
Db 1 AMPESYFNCPDGEYQSNVDCCKTCPSGTFVKAPCKIPHTOGQCEKCHPGFTGKDNGLH 60  
QY 89 DCELCSTCDKDNQNVADCSATSDRKCEQIGLYYYDPKFPESCRPCTKCPQGIPLVQECN 148  
Db 61 DCELCSTCDKDNQNVADCSATSDRKCEQIGLYYYDPKFPESCRPCTKCPQGIPLVQECN 120  
QY 149 STANTVCSVVSNPRNWLFLMLIVFCI 176  
Db 121 STANTVCSVVSNPRNWLFLMLIVFCI 148

RESULT 3  
US-08-292-549-6  
; Sequence 6, Application US/08292549  
; Patent No. 546938  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Goodwin, Raymond G.  
; TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,549  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/963,330  
; FILING DATE: 10/19/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2602-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-292-549-6

Query Match 20.6%; Score 206.5; DB 1; Length 355;  
Best Local Similarity 31.1%; Pred. No. 1.4e-11;  
Matches 55; Conservative 25; Mismatches 72; Indels 25; Gaps 8;  
QY 14 FLLLLLNLFLPV--IFAMPESYFNCPDGEYQSNVDCCKTCPSGTFVKAPC-KIPHTQG 70  
Db 4 YLLLLLSCIIIIINSIDITPHEPSNGCKDNEYKRHHLLCLLSCPPGTYASRLCDSKNTNT 63  
QY 71 QCEKCHPGFTGKDNGLHDELCG--TCDDQNQNVADCSATSDRKCEQIGLYYYDPKFPPE 129  
Db 64 QCTPCASDFTTSRNNHLPACLSGNGRCDNSQVETRSCNTTHNRICDAPG--YYCFLKGS 122  
QY 130 SCRPC---TKC-----PQGIPLVQEC-----NSTANTV--CSSSVSNPRNWL 166  
Db 123 GCKACVSOQKCGIGYGVSGHTPTGDVVCSPCGLGTYSHTVSSVDKCEPVPSTNFNYI 179

RESULT 4  
US-09-006-353A-14  
; Sequence 14, Application US/09006353A  
; Patent No. 6261801  
; GENERAL INFORMATION:  
; APPLICANT: WEI, YING-FEI  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: GENTZ, REINER  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/006,353A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROOKES, ANDERS A.  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF341  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-006-353A-14

Query Match 20.6%; Score 206.5; DB 3; Length 355;  
Best Local Similarity 31.1%; Pred. No. 1.4e-11;  
Matches 55; Conservative 25; Mismatches 72; Indels 25; Gaps 8;  
QY 14 FLLLLLNLFLPV--IFAMPESYFNCPDGEYQSNVDCCKTCPSGTFVKAPC-KIPHTQG 70  
Db 4 YLLLLLSCIIIIINSIDITPHEPSNGCKDNEYKRHHLLCLLSCPPGTYASRLCDSKNTNT 63  
QY 71 QCEKCHPGFTGKDNGLHDELCG--TCDDQNQNVADCSATSDRKCEQIGLYYYDPKFPPE 129  
Db 64 QCTPCASDFTTSRNNHLPACLSGNGRCDNSQVETRSCNTTHNRICDAPG--YYCFLKGS 122  
QY 130 SCRPC---TKC-----PQGIPLVQEC-----NSTANTV--CSSSVSNPRNWL 166

123 GCKACVSTQKCGIGYVSGHTGTGDDVVCSPGGLGTYSHTVSSVDKCEPVPSNTFNFI 179

RESULT 5

US-09-573-986-14

Sequence 14, Application US/09573986

Patent No. 6455040

GENERAL INFORMATION:

APPLICANT: Wei, Ying-Fei

APPLICANT: Ni, Jian

APPLICANT: Gentz, Reiner

APPLICANT: Ruben, Steven

FILE OF INVENTION: Tumor Necrosis Factor Receptor 5

FILE REFERENCE: 1488.1280004

CURRENT APPLICATION NUMBER: US/09/573,986

CURRENT FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 14

LENGTH: 355

TYPE: PRT

ORGANISM: Homo sapiens

US-09-573-986-14

Query Match 20.6%; Score 206.5; DB 4; Length 355;

Best Local Similarity 31.1%; Pred. No. 1.4e-11;

Matches 55; Conservative 25; Mismatches 72; Indels 25; Gaps 8;

QY 14 FLLLLLLNLFV--IFAMPESYFNCNCPDGEYQNDVCKTCPSGTFVKAPC-KIPHTQG 70

DB 4 YLLLLLLSCIIINSIDTPHPSNGKCKDNEYKRHLCLCLSCPPGTVASRLCDKSKTNT 63

QY 71 QCEKCHPGTFTKDNGLHDCELCS-TCDDQNNVADCSATSDRKCEQGLIYYDPKFE 129

DB 64 QCTCASDFTTGRNNHLPACLCNGRCDSNQVETRSCTTHNRICDCAFQ-YVCFKGS 122

QY 130 SCRPC---TKC-----PQGIPLQEC-----NSTANTV--CSSSVSNPRNL 166

DB 123 GCKACVSTQKCGIGYVSGHTGTGDDVVCSPGGLGTYSHTVSSVDKCEPVPSNTFNFI 179

RESULT 6

US-08-050-319B-2

Sequence 2, Application US/08050319B

Patent No. 5633145

GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Necrosis Factor alpha) Receptor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319B

FILING DATE: 10-May-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Robbins, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-050-319B-2

Query Match 20.5%; Score 205.5; DB 1; Length 167;

Best Local Similarity 31.3%; Pred. No. 7.7e-12;

Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

QY 7 VSSLHWFLLLLLLNLF-----PVIFAMP-----ESYFNCNCPGEY---QSNVDCCKTC 53

DB 3 LSTVPDLLPLVLELLLVGYPGVLVPHLGRKRDVCPGKGIHPONNSICCTKC 62

QY 54 PSGTFFVKAPCKIPHTQGCCKCHPTGTGDKNGLHDCELCTCDKQNMV--ADCSATSD 111

DB 63 HKGTLYNDPCPGQDIDCRECESSFTASENHLRHCLSCSKCKEMGOVEISSCTVDRD 122

QY 112 RKCEQIGLY-YDPKFPESCRPCTKCPQGIPLVQECNSTANTVCS 156

DB 123 TVCGCRKNQYRHWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167

RESULT 7

US-08-050-319B-57

Sequence 57, Application US/08050319B

Patent No. 5633145

GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Necrosis Factor alpha) Receptor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319B

FILING DATE: 10-May-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Robbins, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-050-319B-57

Query Match 20.5%; Score 205.5; DB 1; Length 167;

Best Local Similarity 31.3%; Pred. No. 7.7e-12;

Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

QY 7 VSSLHWFLLLLLLNLF-----PVIFAMP-----ESYFNCNCPGEY---QSNVDCCKTC 53

Db 3 LSTVPDLLPLVLELLVGIYPSGVIGLVPHGLDREKRDSCVCPQGYIHPQNNISCTCTKC 62  
QY 54 PSGETFKAPCKIPHTQGCCKHPGTFTGKDNGLHDCELCSTCDKQNNV--ADCSATSD 111  
Db 63 HKGTLYNDPCPGQDTCRECESSGFTASENHLRHCLSCSKCKEMQGVESSTCTVD 122  
QY 112 KRCCEQIGLY-YYPDKFPESCRCPTKCPQGIPLVQECNSTANTVCS 156  
Db 123 TVCGCRKNQRYHYSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167

## RESULT 8

US-08-465-982-2  
; Sequence 2, Application US/08465982  
; Patent No. 5863786  
; GENERAL INFORMATION:  
; APPLICANT: M.Feldmann, P.W. Gray,  
; APPLICANT: M.J.C. Turner, F.M. Brennan  
; TITLE OF INVENTION: Modified human TNFalpha (Tumor  
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robbins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,982  
; FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/050,319  
; FILING DATE: 10-May-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robbins, Roberta L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 5150-0030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 617-8999  
; TELEFAX: (415) 327-3231  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 167 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-465-982-2

Query Match 20.5%; Score 205.5; DB 2; Length 167;  
Best Local Similarity 31.3%; Pred. No. 7.7e-12;  
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

QY 7 VSSLSHWFLLLLNLFL-----PVIFAMP-----ESYFNCPDGEY---QSNVCCCKTC 53  
Db 3 LSTVPDLLPLVLELLVGIYPSGVIGLVPHGLDREKRDSCVCPQGYIHPQNNISCTCTKC 62  
QY 54 PSGETFKAPCKIPHTQGCCKHPGTFTGKDNGLHDCELCSTCDKQNNV--ADCSATSD 111  
Db 63 HKGTLYNDPCPGQDTCRECESSGFTASENHLRHCLSCSKCKEMQGVESSTCTVD 122  
QY 112 KRCCEQIGLY-YYPDKFPESCRCPTKCPQGIPLVQECNSTANTVCS 156  
Db 123 TVCGCRKNQRYHYSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167

## RESULT 9

US-08-465-982-57  
; Sequence 57, Application US/08465982  
; Patent No. 5863786  
; GENERAL INFORMATION:  
; APPLICANT: M.Feldmann, P.W. Gray,  
; APPLICANT: M.J.C. Turner, F.M. Brennan  
; TITLE OF INVENTION: Modified human TNFalpha (Tumor  
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robbins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,982  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/050,319  
; FILING DATE: 10-May-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robbins, Roberta L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 5150-0030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 617-8999  
; TELEFAX: (415) 327-3231  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 167 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-465-982-57

Query Match 20.5%; Score 205.5; DB 2; Length 167;  
Best Local Similarity 31.3%; Pred. No. 7.7e-12;  
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

QY 7 VSSLSHWFLLLLNLFL-----PVIFAMP-----ESYFNCPDGEY---QSNVCCCKTC 53  
Db 3 LSTVPDLLPLVLELLVGIYPSGVIGLVPHGLDREKRDSCVCPQGYIHPQNNISCTCTKC 62  
QY 54 PSGETFKAPCKIPHTQGCCKHPGTFTGKDNGLHDCELCSTCDKQNNV--ADCSATSD 111  
Db 63 HKGTLYNDPCPGQDTCRECESSGFTASENHLRHCLSCSKCKEMQGVESSTCTVD 122  
QY 112 KRCCEQIGLY-YYPDKFPESCRCPTKCPQGIPLVQECNSTANTVCS 156  
Db 123 TVCGCRKNQRYHYSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167

## RESULT 10

US-08-828-683A-21  
; Sequence 21, Application US/0828683A  
; Patent No. 6469144  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco



[illegible]



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2003, 13:24:38 ; Search time 39.6543 Seconds  
(without alignments)  
585.693 Million cell updates/sec

Title: US-09-855-266A-1

Perfect score: 1000

Sequence: 1 MVTFSHVSSLHSHWFLLLLL.....SSVSNRNWFLMLLIVFCI 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 497079 segs, 131961718 residues

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pap:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pap:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pap:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pap:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pap:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pap:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pap:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pap:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pap:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pap:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1000	100.0	176	10	US-09-855-266A-1
2	1000	100.0	176	15	US-10-193-616-8
3	917	91.7	396	15	US-10-193-616-14
4	858	85.8	148	10	US-09-855-266A-2
5	668	66.8	117	15	US-10-193-616-6
6	215.5	21.6	247	15	US-10-193-616-10
7	213.5	21.3	162	9	US-09-798-789-13
8	213.5	21.3	162	16	US-10-218-102-423
9	212.5	21.2	123	10	US-09-855-266A-13
10	209	20.9	461	9	US-09-899-422-15
11	209	20.9	461	10	US-09-898-234-15
12	209	20.9	461	10	US-09-899-429A-25
13	209	20.9	461	10	US-09-792-356-15
14	207.5	20.8	162	9	US-09-798-789-15
15	207.5	20.8	162	16	US-10-218-102-425

16	206.5	20.6	355	9	US-09-826-212-14	Sequence 14, Appl
17	206.5	20.6	355	10	US-09-935-727-16	Sequence 16, Appl
18	206.5	20.6	355	15	US-10-186-643-14	Sequence 14, Appl
19	205.5	20.5	197	14	US-10-112-793-21	Sequence 21, Appl
20	205.5	20.5	201	10	US-09-899-429A-14	Sequence 14, Appl
21	205.5	20.5	211	10	US-09-899-429A-8	Sequence 8, Appl
22	205.5	20.5	213	14	US-10-125-062-1	Sequence 1, Appl
23	205.5	20.5	371	9	US-09-899-422-12	Sequence 12, Appl
24	205.5	20.5	371	10	US-09-898-234-12	Sequence 12, Appl
25	205.5	20.5	371	10	US-09-792-356-12	Sequence 12, Appl
26	205.5	20.5	455	9	US-09-826-212-3	Sequence 3, Appl
27	205.5	20.5	455	9	US-09-333-966-5	Sequence 5, Appl
28	205.5	20.5	455	9	US-09-027-287-3	Sequence 3, Appl
29	205.5	20.5	455	9	US-09-874-138-3	Sequence 3, Appl
30	205.5	20.5	455	9	US-09-840-707A-16	Sequence 16, Appl
31	205.5	20.5	455	9	US-09-252-656B-3	Sequence 3, Appl
32	205.5	20.5	455	9	US-09-899-422-2	Sequence 2, Appl
33	205.5	20.5	455	9	US-09-899-422-17	Sequence 17, Appl
34	205.5	20.5	455	10	US-09-935-727-5	Sequence 5, Appl
35	205.5	20.5	455	10	US-09-898-234-2	Sequence 2, Appl
36	205.5	20.5	455	10	US-09-898-234-17	Sequence 17, Appl
37	205.5	20.5	455	10	US-09-756-854-5	Sequence 5, Appl
38	205.5	20.5	455	10	US-09-899-429A-2	Sequence 2, Appl
39	205.5	20.5	455	10	US-09-899-429A-27	Sequence 27, Appl
40	205.5	20.5	455	10	US-09-792-356-2	Sequence 2, Appl
41	205.5	20.5	455	11	US-09-792-356-17	Sequence 17, Appl
42	205.5	20.5	455	11	US-09-314-889-5	Sequence 5, Appl
43	205.5	20.5	455	13	US-10-005-842-3	Sequence 3, Appl
44	205.5	20.5	455	14	US-10-120-397-2	Sequence 2, Appl
45	205.5	20.5	455	14	US-10-041-574-5	Sequence 5, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-855-266A-1  
; Sequence 1, Application US/09855266A  
; Patent No. US20020128435A1  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501-040002  
; CURRENT APPLICATION NUMBER: US/09/855,266A  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 09/411,722  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-855-266A-1

Query Match	100.0%	Score 1000;	DB 10;	Length 176;
Best Local Similarity	100.0%	Pred. No. 3.1e-85;		
Matches 176;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MVTFSHVSSLHSHWFLLLLLLLFLPVIFAMPEYSFNC PDGEYQSDNVCCKTCPSGTGFK 60		
Db	1	MVTFSHVSSLHSHWFLLLLLLLFLPVIFAMPEYSFNC PDGEYQSDNVCCKTCPSGTGFK 60		
Qy	61	APCKIPHTQGQCEKCHFGFTTGGKDNGLHDCSTCKDQNNVADCSATSDRKCEQIGL 120		
Db	61	APCKIPHTQGQCEKCHFGFTTGGKDNGLHDCSTCKDQNNVADCSATSDRKCEQIGL 120		
Qy	121	YYDPKPFESCRPCTKCPQGIPLVQECNSTANTVCCSSSVSNRNWFLMLLIVFCI 176		



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Db      121 YYDPKFPESCRPCTKCPQIPVLOECNSTANTVCSVSNRNWFLMLLVFCI 176
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RESULT 2
US-10-193-616-8
; Sequence 8, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymk25, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-193-616-8

Query Match      100.0%; Score 1000; DB 15; Length 176;
Best Local Similarity 100.0%; Pred. No. 3.1e-85;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MVTFSVSSLSHWFLLLLNLFLPVIFAMPESYFNCPDGEYQSNVCCKTCPSGTFVK 60
Db      1 MVTFSVSSLSHWFLLLLNLFLPVIFAMPESYFNCPDGEYQSNVCCKTCPSGTFVK 60
Qy      61 APCIPHTQGCCKCHPGTFTGKDNGLHDCCLSTCDKDNVADCSATSDRKCEQIGL 120
Db      61 APCIPHTQGCCKCHPGTFTGKDNGLHDCCLSTCDKDNVADCSATSDRKCEQIGL 120
Qy      121 YYDPKFPESCRPCTKCPQIPVLOECNSTANTVCSVSNRNWFLMLLVFCI 176
Db      121 YYDPKFPESCRPCTKCPQIPVLOECNSTANTVCSVSNRNWFLMLLVFCI 176
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RESULT 3
US-10-193-616-14
; Sequence 14, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymk25, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: ymk25-Fc fusion protein
US-10-193-616-14

Query Match      91.7%; Score 917; DB 15; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.6e-77;
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Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MVTFSVSSLSHWFLLLLNLFLPVIFAMPESYFNCPDGEYQSNVCCKTCPSGTFVK 60
Qy      61 APCIPHTQGCCKCHPGTFTGKDNGLHDCCLSTCDKDNVADCSATSDRKCEQIGL 120
Db      61 APCIPHTQGCCKCHPGTFTGKDNGLHDCCLSTCDKDNVADCSATSDRKCEQIGL 120
Qy      121 YYDPKFPESCRPCTKCPQIPVLOECNSTANTVCSVSNRNWFLMLLVFCI 161
Db      121 YYDPKFPESCRPCTKCPQIPVLOECNSTANTVCSVSNRNWFLMLLVFCI 161
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RESULT 4
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

Query Match      85.8%; Score 858; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.7e-72;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      29 AMPESYFNCPDGEYQSNVCCKTCPSGTFVRAKPIHTQGCCKCHPGTFTGKDNGLH 88
Db      1 AMPESYFNCPDGEYQSNVCCKTCPSGTFVRAKPIHTQGCCKCHPGTFTGKDNGLH 60
Qy      89 DCELCSTCDKDNVADCSATSDRKCEQIGLYYYDPKFPESCRPCTKCPQIPVLOECN 148
Db      61 DCELCSTCDKDNVADCSATSDRKCEQIGLYYYDPKFPESCRPCTKCPQIPVLOECN 120
Qy      149 STANTVCSVSNRNWFLMLLVFCI 176
Db      121 STANTVCSVSNRNWFLMLLVFCI 148
|||||
RESULT 5
US-10-193-616-6
; Sequence 6, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymk25, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
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, PRIOR APPLICATION NUMBER: 08/383,676
,
, PRIOR FILING DATE: 1995-02-01
,
, PRIOR APPLICATION NUMBER: 08/153,287
,
, PRIOR FILING DATE: 1993-11-17
,
, PRIOR APPLICATION NUMBER: 07/821,750
,
, PRIOR FILING DATE: 1992-01-02
,
, PRIOR APPLICATION NUMBER: 07/511,430
,
, PRIOR FILING DATE: 1990-04-20
,
, NUMBER OF SEQ ID NOS: 87
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, SOFTWARE: PatentIn ver. 2.0
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, SEQ ID NO 15
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, LENGTH: 461
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, TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8
US-09-899-422-15
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Query Watch              20.9%; Score 209; DB 9; Length 461;
Best Local Similarity 27.4%; Pred. No. 1.8e-11;
Matches 52; Conservative 22; Mismatches 62; Indels 54; Gaps 7;

QY 38 CPDGEY---QSDNVCCCTCPSGTFVKAPCKPIPHQTQGCERKCHPGTFTGDKNGLHDCELCS 94
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QY 95 TCDKD---QNVVADCATSDRKCEC---QIGLYYDPKFPESCRCPTKCPGPIPVQECNS 149
Db 104 TCRKEMFQVEISPCKADMDTVCGCKKNQFORYLSETHF---QCVDSCPCFNG-TVTIPCKE 160
QY 150 TANTVCS-----SSVSNPRN-----WL 166
Db 161 KQTVNCNCHAGFFLGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGAVLLPIVIFL 220
QY 167 FLMLIVFCI 176
Db 221 GLCLLFFICI 230

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RESULT 11
US-09-898-234-15
; Sequence 15, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmier, Adolph
; APPLICANT: Maurer-Fog, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15

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/ PRIOR FILING DATE: 1993-02-01
/ PRIOR APPLICATION NUMBER: 08/153,287
/ PRIOR FILING DATE: 1993-11-17
/ PRIOR APPLICATION NUMBER: 07/821,750
/ PRIOR FILING DATE: 1992-01-02
/ PRIOR APPLICATION NUMBER: 07/511,430
/ PRIOR FILING DATE: 1990-04-20
/ NUMBER OF SEQ ID NOS: 87
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 461
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8
US-09-898-234-15

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	858	100.0	148	3	US-09-411-722-2	Sequence 2, Appli	
2	858	100.0	176	3	US-09-411-722-1	Sequence 1, Appli	
3	205	23.9	327	3	US-09-290-640-66	Sequence 66, Appli	
4	204.5	23.8	285	3	US-08-804-166-6	Sequence 6, Appli	
5	204.5	23.8	285	3	US-08-910-991-6	Sequence 6, Appli	
6	200.5	23.4	139	4	US-08-706-945D-129	Sequence 129, App	
7	200.5	23.4	153	2	US-08-219-2378-A	Sequence 4, Appli	
8	200.5	23.4	153	3	US-08-477-347-12	Sequence 12, Appli	
9	200.5	23.4	153	3	US-08-476-862-3	Sequence 3, Appli	
10	200.5	23.4	153	3	US-08-468-560C-4	Sequence 4, Appli	
11	200.5	23.4	153	4	US-09-800-909-3	Sequence 3, Appli	
12	200.5	23.4	154	4	US-08-828-683A-12	Sequence 12, Appli	
13	200.5	23.4	161	4	US-09-326-394-2	Sequence 2, Appli	
14	200.5	23.4	167	1	US-08-050-319B-2	Sequence 2, Appli	
15	200.5	23.4	167	1	US-08-050-319B-57	Sequence 57, Appli	
16	200.5	23.4	167	2	US-08-465-982-2	Sequence 2, Appli	
17	200.5	23.4	167	2	US-08-465-982-57	Sequence 57, Appli	
18	200.5	23.4	197	4	US-08-828-683A-21	Sequence 21, Appli	
19	200.5	23.4	256	3	US-08-804-166-2	Sequence 2, Appli	
20	200.5	23.4	256	3	US-08-910-991-2	Sequence 2, Appli	
21	200.5	23.4	280	3	US-08-974-022-46	Sequence 46, Appli	
22	200.5	23.4	280	3	US-08-795-445A-46	Sequence 46, Appli	
23	200.5	23.4	280	3	US-08-795-447A-46	Sequence 46, Appli	
24	200.5	23.4	280	3	US-08-974-186-46	Sequence 46, Appli	
25	200.5	23.4	280	3	US-08-795-446B-46	Sequence 46, Appli	
26	200.5	23.4	280	4	US-08-706-945D-132	Sequence 132, App	
27	200.5	23.4	307	3	US-08-804-166-4	Sequence 4, Appli	

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; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-1

Query Match      100.0%; Score 858; DB 3; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.9e-74;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMPESYFNCNCPDGEYQSNVCCVCTPSGTFVKAPCKIPHTQOCEKCHPGTGTGKDNGLH 60
DB 1 AMPESYFNCNCPDGEYQSNVCCVCTPSGTFVKAPCKIPHTQOCEKCHPGTGTGKDNGLH 88
QY 61 DCELCSTCDKQNMVADCSATSDRKCEQIGLYYDPPKPEPCRCPTKCPQGIPIVLOECN 120
DB 89 DCELCSTCDKQNMVADCSATSDRKCEQIGLYYDPPKPEPCRCPTKCPQGIPIVLOECN 148
QY 121 STANTVCSSVSNNRNWFLMLIVFCI 148
DB 149 STANTVCSSVSNNRNWFLMLIVFCI 176

RESULT 3
US-09-290-640-66
; Sequence 66, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-290-640-66

Query Match      23.9%; Score 205; DB 3; Length 327;
Best Local Similarity 31.5%; Pred. No. 5.1e-12;
Matches 45; Conservative 23; Mismatches 67; Indels 8; Gaps 5;

QY 9 NCPDGEYQSNVCCVCTPSGTFVKAPCKIPHTQOCEKCHPG-TFTGKDNGLHDCELST 67
DB 43 NCSEGLYGGPPCCQPCQPCQKXKEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTL 102
QY 68 CDKDNMVD--CSATSDRKCEQIGLYYDPPKPEPCRCPTKCPQGIPIVLOECNSTANT 125
DB 103 CDEEHGLEVEYNTLTONTKCKKPD-FYCDSPGCEHCVRASCERH--TLEPCTATSWT 159
QY 126 VCSSVSNNRNWFLMLIVFCI 148
DB 160 NCRK--QSPRNRLWLLTILVLLI 180

RESULT 4
US-08-804-166-6
; Sequence 6, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
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; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-804-166-6

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Best Local Similarity 34.4%; Pred. No. 4.9e-12;
Matches 43; Conservative 15; Mismatches 60; Indels 7; Gaps 4;

QY 10 CPDGEY---OSNDVCCVCTPSGTFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCS 66
DB 26 CPQGIPIVLOECNSTANT 125
QY 67 TCDKQNMV--ADCSATSDRKCEQIGLY-YDPPKPEPCRCPTKCPQGIPIVLOECNSTA 123
DB 86 KCRKEMGQVEISSCTVDRTVCGCRKNQYRHWSENLFQCFNCTCLNG-TVHLSCQEQK 144
QY 124 NTVCS 128
DB 145 NTVCT 149

RESULT 5
US-08-910-991-6
; Sequence 6, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
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RESULT 9  
US-08-476-862-3  
; Sequence 3, Application US/08476862  
; Patent No. 6262239  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BIGDA, Jacek

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RESULT 10
US-08-468-560C-4
; Sequence 4, Application US/08468560C
; Patent No. 6270998
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto

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1  RESULT 11
2  US-09-800-909-3
3  Sequence 3, Application US/09800909
4  Patent No. 655111
5  GENERAL INFORMATION:
6  APPLICANT: WALLACH, David
7  APPLICANT: BIGDA, Jacek
8  APPLICANT: BELETSKY, Igor
9  APPLICANT: METT, Igor
10 APPLICANT: ENGELMANN, Hartmut
11 TITLE OF INVENTION: TNF INHIBITORS
12 NUMBER OF SEQUENCES: 8
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: BROWDY AND NEIMARK
15 STREET: 419 Seventh Street, N.W.
16 CITY: Washington
17 STATE: D.C.
18 COUNTRY: USA
19 ZIP: 20004
20 COMPUTER READABLE FORM:

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RESULT 12
US-08-828-683A-12
; Sequence 12, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

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PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/036,355

\* TYPE: amino acid

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; TYPE: amino acid

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2003, 13:24:38 ; Search time 33.3457 Seconds  
(without alignments)  
585.693 Million cell updates/sec

Title: US-09-855-266A-2

Perfect score: 858

Sequence: 1 AMPESYFNCPDGEYQSNV.....SSVSNRNWFLMLIVFCI 148

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Total number of hits satisfying chosen parameters: 497079

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	858	100.0	148	10	US-09-855-266A-2
2	858	100.0	176	15	US-09-855-266A-1
3	858	100.0	176	15	US-10-193-616-8
4	775	90.3	396	15	US-10-193-616-14
5	526	61.7	117	15	US-10-193-616-6
6	215.5	25.1	247	15	US-10-193-616-10
7	213.5	24.9	162	9	US-09-798-789-13
8	213.5	24.9	162	16	US-10-218-102-423
9	212.5	24.8	123	10	US-09-855-266A-13
10	209	24.4	461	9	US-09-899-422-15
11	209	24.4	461	10	US-09-898-234-15
12	209	24.4	461	10	US-09-899-429A-25
13	209	24.4	461	10	US-09-792-356-15
14	207.5	24.2	162	9	US-09-798-789-15
15	207.5	24.2	162	16	US-10-218-102-425

16	205	23.9	204	10	US-09-948-018-18
17	205	23.9	242	15	US-10-193-616-9
18	205	23.9	327	9	US-09-802-669-66
19	204.5	23.8	162	9	US-09-798-789-20
20	204.5	23.8	162	16	US-10-218-102-430
21	204.5	23.8	285	9	US-09-756-186-6
22	203.5	23.7	162	9	US-09-798-789-19
23	203.5	23.7	162	16	US-10-218-102-429
24	202.5	23.6	162	9	US-09-798-789-11
25	202.5	23.6	162	16	US-10-218-102-421
26	201.5	23.5	162	9	US-09-798-789-14
27	201.5	23.5	162	16	US-10-218-102-424
28	200.5	23.4	153	9	US-09-800-909-3
29	200.5	23.4	153	10	US-09-884-987-4
30	200.5	23.4	153	10	US-09-800-908-12
31	200.5	23.4	154	14	US-10-112-793-12
32	200.5	23.4	161	9	US-09-899-422-4
33	200.5	23.4	161	10	US-09-907-263-2
34	200.5	23.4	161	10	US-09-898-234-4
35	200.5	23.4	161	10	US-09-899-429A-4
36	200.5	23.4	161	10	US-09-792-356-4
37	200.5	23.4	161	11	US-09-882-735-2
38	200.5	23.4	162	9	US-09-798-789-9
39	200.5	23.4	162	9	US-09-798-789-21
40	200.5	23.4	162	9	US-09-798-789-22
41	200.5	23.4	162	10	US-09-899-429A-6
42	200.5	23.4	162	11	US-09-852-455-5
43	200.5	23.4	162	16	US-10-218-102-419
44	200.5	23.4	162	16	US-10-218-102-431
45	200.5	23.4	162	16	US-10-218-102-432

#### ALIGNMENTS

#### RESULT 1

US-09-855-266A-2  
; Sequence 2, Application US/09855266A  
; Patent No. US20020128435A1  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501-040002  
; CURRENT APPLICATION NUMBER: US/09/855,266A  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 09/411,722  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JF98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-855-266A-2

Query Match	100.0%;	Score 858;	DB 10;	Length 148;
Best Local Similarity	100.0%;	Pred. No. 1.5e-72;		
Matches 148;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	AMPESYFNCPDGEYQSNVCCCKTCSGTFVKAPCKIPHTQGCQCEKCHPGFTTKDNGLH 60		
Db	1	AMPESYFNCPDGEYQSNVCCCKTCSGTFVKAPCKIPHTQGCQCEKCHPGFTTKDNGLH 60		
QY	61	DCELSTCDKQDNVADCSATSDRKCEQGLIYYDFKFFPESCRPCTKCPGIPVLQECN 120		
Db	61	DCELSTCDKQDNVADCSATSDRKCEQGLIYYDFKFFPESCRPCTKCPGIPVLQECN 120		
QY	121	STANTVCCSSVSNRNWFLMLIVFCI 148		

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Db      121 STANTVCSSSVSNPRNWLFLMLLVFCI 148
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US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-1

Query Match      100.0%; Score 858; DB 10; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AMPESYFNCPDGEYQSDVCKTCPSGTFVKA CKIPHTQGCCKCHPGFTFGKDNGLH 60
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Db      29  AMPESYFNCPDGEYQSDVCKTCPSGTFVKA CKIPHTQGCCKCHPGFTFGKDNGLH 88
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Qy      61  DCELCSTCDKQNMVADCSATSDRKCECQIGLYYYDPKFPESCRCRPTCKPQGIPLVQECN 120
|||||
Db      89  DCELCSTCDKQNMVADCSATSDRKCECQIGLYYYDPKFPESCRCRPTCKPQGIPLVQECN 148
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Qy      121 STANTVCSSSVSNPRNWLFLMLLVFCI 148
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Db      149 STANTVCSSSVSNPRNWLFLMLLVFCI 176
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RESULT 4
US-10-193-616-14
; Sequence 14, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: ymkz5-Fc fusion protein
US-10-193-616-14

Query Match      90.3%; Score 775; DB 15; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      29  AMPESYFNCPDGEYQSDVCKTCPSGTFVKA CKIPHTQGCCKCHPGFTFGKDNGLH 88
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Qy      61  DCELCSTCDKQNMVADCSATSDRKCECQIGLYYYDPKFPESCRCRPTCKPQGIPLVQECN 120
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Db      89  DCELCSTCDKQNMVADCSATSDRKCECQIGLYYYDPKFPESCRCRPTCKPQGIPLVQECN 148
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Qy      121 STANTVCSSSVSN 133
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Db      149 STANTVCSSSVSN 161
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RESULT 5
US-10-193-616-6
; Sequence 6, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07

Query Match      100.0%; Score 858; DB 15; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      29  AMPESYFNCPDGEYQSDVCKTCPSGTFVKA CKIPHTQGCCKCHPGFTFGKDNGLH 88
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Qy      61  DCELCSTCDKQNMVADCSATSDRKCECQIGLYYYDPKFPESCRCRPTCKPQGIPLVQECN 120
|||||
Db      89  DCELCSTCDKQNMVADCSATSDRKCECQIGLYYYDPKFPESCRCRPTCKPQGIPLVQECN 148
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Qy      121 STANTVCSSSVSNPRNWLFLMLLVFCI 148
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Db      149 STANTVCSSSVSNPRNWLFLMLLVFCI 176
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RESULT 3
US-10-193-616-8
; Sequence 8, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-193-616-8

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Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      124 NTVCT 128

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RESULT 15
US-10-218-102-425
; Sequence 425, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmeiter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-10

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Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1000	37.0	176	3	US-09-411-722-1
2	858	31.7	148	3	US-09-411-722-2
3	207.5	7.7	280	3	US-08-974-022-46
4	207.5	7.7	280	3	US-08-795-445A-46
5	207.5	7.7	280	3	US-08-795-447A-46
6	207.5	7.7	280	3	US-08-974-186-46
7	207.5	7.7	280	3	US-08-795-446B-46
8	207.5	7.7	280	4	US-08-706-945D-132
9	207.5	7.7	455	1	US-08-050-319B-25
10	207.5	7.7	455	1	US-08-321-668-2
11	207.5	7.7	455	1	US-08-837-941-2
12	207.5	7.7	455	2	US-08-126-016-2

13	207.5	7.7	455	2	US-08-465-982-25	Sequence 25, Appl
14	207.5	7.7	455	3	US-08-815-469-5	Sequence 5, Appl
15	207.5	7.7	455	3	US-09-006-353A-3	Sequence 3, Appl
16	207.5	7.7	455	4	US-09-527-236A-5	Sequence 5, Appl
17	207.5	7.7	455	4	US-08-054-970-2	Sequence 2, Appl
18	207.5	7.7	455	4	US-09-565-918-4	Sequence 4, Appl
19	207.5	7.7	455	4	US-09-573-986-3	Sequence 3, Appl
20	207.5	7.7	455	4	US-09-027-287-3	Sequence 3, Appl
21	207.5	7.7	455	4	US-09-252-656B-3	Sequence 3, Appl
22	207.5	7.7	455	4	US-08-406-824A-4	Sequence 4, Appl
23	206.5	7.6	355	1	US-08-292-549-6	Sequence 6, Appl
24	206.5	7.6	355	3	US-09-006-353A-14	Sequence 14, Appl
25	206.5	7.6	355	4	US-09-573-986-14	Sequence 14, Appl
26	205.5	7.6	167	1	US-08-050-319B-2	Sequence 2, Appl
27	205.5	7.6	167	1	US-08-050-319B-57	Sequence 57, Appl
28	205.5	7.6	167	2	US-08-465-982-2	Sequence 2, Appl
29	205.5	7.6	167	2	US-08-465-982-57	Sequence 57, Appl
30	205.5	7.6	197	4	US-08-828-683A-21	Sequence 21, Appl
31	205	7.6	327	3	US-09-290-640-66	Sequence 66, Appl
32	204.5	7.6	199	1	US-08-050-319B-48	Sequence 48, Appl
33	204.5	7.6	199	2	US-08-465-982-48	Sequence 48, Appl
34	204.5	7.6	285	3	US-08-804-166-6	Sequence 6, Appl
35	204.5	7.6	285	3	US-08-910-991-6	Sequence 6, Appl
36	202.5	7.5	349	3	US-09-006-353A-13	Sequence 13, Appl
37	202.5	7.5	349	4	US-09-573-986-13	Sequence 13, Appl
38	202.5	7.5	426	4	US-08-747-562-37	Sequence 37, Appl
39	201	7.4	909	4	US-09-013-895A-4	Sequence 4, Appl
40	201	7.4	909	4	US-09-448-868-4	Sequence 4, Appl
41	200.5	7.4	139	4	US-08-706-945D-129	Sequence 129, App
42	200.5	7.4	153	2	US-08-219-237B-4	Sequence 4, Appl
43	200.5	7.4	153	3	US-08-477-347-12	Sequence 12, Appl
44	200.5	7.4	153	3	US-08-476-862-3	Sequence 3, Appl
45	200.5	7.4	153	3	US-08-468-560C-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-09-411-722-1  
; Sequence 1, Application US/09411722  
; Patent No. 6271366  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501/040001  
; CURRENT APPLICATION NUMBER: US/09/411.722  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-411-722-1

Alignment Scores:  
Pred. No.: 6.91e-107 Length: 176  
Score: 1000.00 Matches: 176  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.98% Indels: 0  
DB: 3 Gaps: 0

US-09-855-266A-3 (1-1509) x US-09-411-722-1 (1-176)

QY 12 ATGTTACCTTCACGCCACGCTCCAGTCTGAGTCACGTGGTTCCTGCTGCTGTGTG 71  
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Db 1 MetValThrPheSerHisValSerSerLeuSerHisrrpPheLeuLeuLeuLeuLeu 20

QY 72 AATCTGTTCTGCGGTAATATTGCTGATGCTGAATCATACTCTCTCAACTGTCCTCCCAT 131  
Db 21 AsnLeuPheLeuProValIlePheAlaMetProGluSerTyrSerPheAsnCysProAsp 40  
QY 132 GGTGAATACCACTGCTAATGATGCTGTGCAAGACCTGCTCCCTCAGGTACATTTCTCAAG 191  
Db 41 GlyIuTyrGlnSerAsnAspValCysCysLysThrCysProSerGlyThrPheValLys 60  
QY 192 GCGCCTGCAAAATCCCCCTACTCAAGGACAATGTGAGAAAGTGTACCCAGGACAATTC 251  
Db 61 AlaProCysLysIleProHisThrGlnGlyCysGluLysCysHisProGlyThrPhe 80  
QY 252 ACAGGAAAGATGATGCTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311  
Db 81 ThrGlyLysAspAsnGlyLeuHisAspCysGluLeuCysSerThrCysAspLysAspGln 100  
QY 312 AATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371  
Db 101 AsnMetValAlaAspCysSerAlaThrSerAspArgLysCysGluCysGlnIleGlyLeu 120  
QY 372 TACTACTATGACCCCAAAATTTCCGGAATCATGCGCCCATGTACCAAGTGTCCCAAGGA 431  
Db 121 TyrTyrTyrAspProLysPheProGluSerCysArgProCysThrLysCysProGlnGly 140  
QY 432 ATCCCTGCTCCTCAGGAATGCAACTCCACAGCTAACAGTGTGTCAGTTCTCTTTCA 491  
Db 141 IleProValLeuGlnGluCysAsnSerThrAlaAsnThrValCysSerSerValSer 160  
QY 492 AATCCCAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539  
Db 161 AsnProArgAsnTrpLeuPheLeuLeuMetIleValPheCysIle 176

## RESULT 2

US-09-411-722-2  
; Sequence 2, Application US/09411722  
; Patent No. 6271366  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501/040001  
; CURRENT APPLICATION NUMBER: US/09/411,722  
; CURRENT FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-411-722-2

## Alignment Scores:

Pred. No.:	1,72e-90	Length:	148
Score:	858.00	Matches:	148
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	31.73%	Indels:	0
DB:	3	Gaps:	0

US-09-855-266A-3 (1-1509) x US-09-411-722-2 (1-148)

QY 96 GCTATGCTGAATCATACTCTTCAACTGCTCCGATGCTGAATACCACTGCTAATGATGTC 155  
Db 1 AlaMetProGluSerTyrSerPheAsnCysProAspGlyGluTyrGlnSerAsnAspVal 20  
QY 156 TGTTCAGACCTGCTGCTCCTCAGGTACATTTGTCAAGCGCCCTGCAAAATCCCATACT 215  
Db 21 CysCysLysThrCysProSerGlyThrPheValLysAlaProCysLysIleProHisThr 40

QY 216 CAAGGAAATGTGAGAAAGTGTCCACGAGAACATTCACAGGAAAGATATATGCTGCTGAT 275  
Db 41 GlnGlyGlnCysGluLysCysHisProGlyThrPheThrGlyLysAspAsnGlyLeuHis 60  
QY 276 GATTGTGAACCTTGTGCTCCACCTGCTGATAAGACCAAGATATGCTGCTGCTGCTGCTGCT 335  
Db 61 AspCysGluLeuCysSerThrCysAspLysAspGlnAsnMetValAlaAspCysSerAla 80  
QY 336 ACCAGTACCGGAAATGCGAGTCCCAAAATAGGTCTTTTACTACTATGACCCCAAAATTTCCG 395  
Db 81 ThrSerAspArgLysCysGluCysGlnIleGlyLeuTyrTyrTrpAspProLysPhePro 100  
QY 396 GAATCATGCGCCCATGTACCAAGTGTCCCAAGGAATCCCTGCTCCTCCAGGAATGCAAC 455  
Db 101 GluSerCysArgProCysThrLysCysProGlnGlyIleProValLeuGlnGluCysAsn 120  
QY 456 TCCACAGCTAACACCTGCTGCGAGTTCATCTGTTTCAAAATCCCAAGAACTGCTGCTGCT 515  
Db 121 SerThrAlaAsnThrValCysSerSerValSerAsnProArgAsnTrpLeuPheLeu 140  
QY 516 CTGATGCTAATGCTCTCTCTGATC 539  
Db 141 LeuMetLeuIleValPheCysIle 148

## RESULT 3

US-08-974-022-46  
; Sequence 46, Application US/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,022  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-974-022-46

## Alignment Scores:

Pred. No.:	4,74e-15	Length:	280
Score:	207.50	Matches:	65
Percent Similarity:	42.13%	Conservative:	26
Best Local Similarity:	30.09%	Mismatches:	95
Query Match:	7.67%	Indels:	30

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?
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/577,788
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Winter, Robert B.
? REFERENCE/DOCKET NUMBER: A-378
? INFORMATION FOR SEQ ID NO: 46:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 280 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-795-445A-46

Alignment Scores:
Pred. No.: 4,74e-15 Length: 280
Score: 207.50 Matches: 65
Percent Similarity: 42.13% Conservative: 26
Best Local Similarity: 30.09% Mismatches: 95
Query Match: 7.67% Indels: 30
DB: 3 Gaps: 7

US-09-855-266A-3 (1-1509) x US-08-795-445A-46 (1-280)

QY 30 GTCTCCAGTCTGAGTCACACTGGTTCCTCTGTCTGTCTGTCTGTGAATCTGTCTTGTG----- 83
   :::::
Db 3 LeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuLeuGluLeuValGlyIle 22
   :::::

QY 84 -----CGGTAATAATTGTGTCATGCCCT-----GAATCATACTCCTTC 119
   |||||
Db 23 TyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluIysArgAspSer 42
   |||||

QY 120 AACTGTCCCGATGGTGAATAC-----CAGTCTAATGATGTCTCTTCTGCAAGACCTGT 170
   |||||
Db 43 ValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThrLysCys 62
   |||||

QY 171 CCCTCAGGTACATTTGTCAAGGGGCCCTGCAAAATCCCCCATACTCAAGGACAACTGTGAG 230
   |||||
Db 63 HisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArg 82
   |||||

QY 231 AAGTGTCAACCCAGACATTACACAGGAAAGAAATAATGGCCCTGCATGATTGTGAACTTTGC 290
   ::|||
Db 83 GluCysGluSerGlySerPheThrAlaSerGluAlaHisLeuArgHisCysLeuSerCys 102
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QY    291   TCACCCCTTGATAAAGACCAGAATATGGTG-----GCTGACGTGTTCTGCCACCGAGNAC   344  
        |||    ||||::    :    :    :    :    :    :    :    :    :    :    :    :    :  
 Db    103   SerLysCysArgIysGIuMetGIyGlnValCIuIfleSerSeryCysThrValAspArgasp   122  
        |||    ||||::    :    :    :    :    :    :    :    :    :    :    :    :  
 QY    345   CGGNAATGCCAGTGCCEAATAGGTCTTTAC---TACTATGACCACCAAAATTCCTCGGAATCA   401  
        |||    ||||::    :    :    :    :    :    :    :    :    :    :    :    :  
 Db    123   ThrValCysGLyCysArgIysAsnGlnItyrArgHisIyrTrpSerGIuAsnLeuPheGln   142  
        |||    ||||::    :    :    :    :    :    :    :    :    :    :    :    :  
 QY    402   TGGCGCCCATGTACCAAGTGTCCCAGAGGAATCCCTGCTCCAGGAATCCAACCTCCACA   461  
        |||    ||||::    :    :    :    :    :    :    :    :    :    :    :    :  
 Db    143   CysPheasnCysSerLeuCysLeuAsnGly---ThrValHisLeuSerCysGlnGIuLys   161  
        |||    ||||::    :    :    :    :    :    :    :    :    :    :    :    :  
 QY    462   GCTAACACTGTGTCAGTCTCA-----TCT   485  
        |||||    |||||::    :    :    :    :    :    :    :    :    :    :    :  
 Db    162   GlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGIuAsnGIuCysValSer   181  
        |||||    |||||::    :    :    :    :    :    :    :    :    :    :    :  
 QY    486   GTTTCAAAATCCCAGAAACTGGCTGTTCCTACTGATGCTAAATTGCTCTCTGTATCTGAAGA   545  
        |||||    ::    :    :    :    :    :    :    :    :    :    :    :    :  
 Db    182   CysSerAsnCysIysIysSerLeuGIuCysThrIysLeuGIuSerCysLeuProGlnIle-GluAs   201  
        |||||    :    :    :    :    :    :    :    :    :    :    :    :  
 QY    546   AGATAAAGGTTCTACAGATGGTGCTCTAGCTTCTCTCTTTTATTTGCTG   591  
        |||||    :    :    :    :    :    :    :    :    :    :    :    :  
 Db    201   nValIysglyThrGluaspserGlyThrThrValLeuLeuproLeu   216  
        |||||    :    :    :    :    :    :    :    :    :    :    :    :

RESULT 5  
RS-08-795-447A-46

DB	QY	QY	QY
103	serLysCysargLysGluMetGlyGlnValGluIleSerCysThrValAspArgasp	122	
345	CGGAAATGCGAGTGGCCAAATAGGCTCTTTAC	---	TACTATGACGCCAAAAATTTCCGGAATCA
30	GTCTCCAGTCTGAGTCTACTGGTTCTCTTCTGCTGCTGCTGAATCTGTCTTG	---	83
3	LeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuValGlyIle	---	22
DB	LeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuValGlyIle	---	22

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; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-446B-46

Alignment Scores:
  Pred. No.:      4,74e-15      Length:      280
  Score:          207.50        Matches:      65
  Percent Similarity: 42.13%    Conservative: 26
  Best Local Similarity: 30.09% Mismatches:   95
  Query Match:      7.67%      Indels:      30
  DB:                7         Gaps:       7

US-09-855-265A-3 (1-1509) x US-08-795-446B-46 (1-280)

QY 30 GTCTCCAGTCTGAGTCACTGGTTCTCTCTCTGCTGCTGAATCTGTCTTTG----- 83
   :::::
Db 3 LeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuValGlyIle 22
   :::::

QY 84 -----CCGGTAATATTTGCTATGCCCT-----GAATCATACTCTCTTC 119
   :::::
Db 23 TyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysAr-gaspSer 42
   :::::

QY 120 AACTGTCGCCGATCGTGAATAC-----CAGTCTAATGATGCTGTGTCGAAGACCTGT 170
   :::::
Db 43 ValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThrLysCys 62
   :::::

QY 171 CCCTCAGTACATTTGTCAAGGGCCCTCGAAAATCCCCATACTCAAGGACAAATGTGAG 230
   :::::
Db 63 HisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArg 82
   :::::

QY 231 AAGTGTACCCAGGAACATTCACAGGAAAGATAATGGCTGCGATGTTGTGAACCTTGC 290
   :::::
Db 83 GluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeuSerCys 102
   :::::

QY 291 TCCACCTGTGATAAAGACCAGCATATGGTG-----GCTGACGTGTTCTGCCACCAGTGAC 344
   :::::
Db 103 SerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAspArgasp 122
   :::::

QY 345 CGGAAATTCGCGAGTGCCAAATAGTCTTTAC---TACTATACGCCAAATTTCCGGGAATCA 401
   :::::
Db 123 ThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeuPheGln 142
   :::::

QY 402 TGGCGGCCCATGTATACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACA 461
   :::::
Db 143 CysPheAsnCysSerLeuLysLeuAsnGly---ThrValHisLeuSerCysGlnGluLys 161
   :::::

QY 462 GCTAAACACGTGTCAGTTCA-----TCT 485
   :::::
Db 162 GlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysValSer 181
   :::::

QY 486 GTTTCAAATCCCAAGAACTGGCTGTTCCTACTGATGCTAATTCCTCTGTATCTGAAGA 545
   :::::
Db 182 CysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIle-GluAs 201
   :::::

QY 546 AGATAAAGGTTTCACAGATGGTGTCTGTAGTCTCTCTTTTATTCGCTG 591
   :::::
Db 201 nValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeu 216
   :::::

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RESULT 8  
US-08-706-945D-132  
: Sequence 132, Application US/08706945D

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; sequence 134, application 0
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Meng-Shi

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## RESULTS





QY 402 TGCCGCCCATGTACCAAGTGTCCCAAGAAATCCCTGCTCCTCCAGGAATGCAACTCCACA 461  
Db 143 CysPheAsnCysSerLeuCysLeuAsnGly---ThrValHisLeuSerCysGlnGluLys 161  
QY 462 GCTAACACTGTGTGAGTTCA-----TCT 485  
Db 162 GlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSer 181  
QY 486 GTTTCAAATCCCAAGAACTGGCTGTCTACTGATGCTAAATGTCTTCTGTATCTGAAGA 545  
Db 182 CysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIle-GluAs 201  
QY 546 AGATAAGGTTCTACAGATGGTGTCTGAGCTTCCTTTATGCTG 591  
Db 201 nValLysGlyThrGluAspSerGlyThrValLeuLeuProLeu 216

## RESULT 10

US-08-321-668-2  
; Sequence 2, Application US/08321668  
; Patent No. 5665859  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BRAKEBUSCH, Cord  
; APPLICANT: VARFOLOMEEV, Eugene  
; APPLICANT: BATKIN, Michael  
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/321,668  
; FILING DATE: 12-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107268  
; FILING DATE: 12-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=13  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633

INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

## US-08-321-668-2

Alignment Scores:  
Pred. No.: 6.15e-15 Length: 455  
Score: 207.50 Matches: 65  
Percent Similarity: 42.13% Conservative: 26  
Best Local Similarity: 30.09% Mismatches: 95  
Query Match: 7.67% Indels: 30  
DB: 1 Gaps: 7

US-09-855-266A-3 (1-1509) x US-08-321-668-2 (1-455)

QY 30 GTCTCCAGTGTGAGTCACTGGTTCCTTCTGCTGCTGCTGAATCTGTTCTTG-----83  
Db 3 LeuSerThrValProAspLeuLeuProLeuValLeuGluLeuLeuValGlyLe 22  
QY 84 -----CCGGTAATATTGTGATGCCCT-----GAATCATATCTCCTTC 119  
Db 23 TyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArgAspSer 42  
QY 120 AACTGTCCCGCATGGTGAATAC-----CAGTCTAATGATGCTGCTTCTCAAGACCTGT 170  
Db 43 ValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysThrLysCys 62  
QY 171 CCCTCAGGTACATTGTCAAGGCGCCCTGCAAAATCCCATCTACTCAAGGACAATGTGAG 230  
Db 63 HisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArg 82  
QY 231 AAGTGTCAACCCAGAACATTCACAGGAAGAAATAAGCTGCTGATGATGTTGTAACCTTGC 290  
Db 83 GluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeuSerCys 102  
QY 291 TCCACCTGTGATAAAGACCAAGATATGGTG-----GCTGACTGTTCTGCCACCAAGAC 344  
Db 103 SerLysCysArgLysGluMetGlyGlnValGluLeuSerSerCysThrValAspArgAsp 122  
QY 345 CGGAAATGCGAGTGCACCAATAGGTCTTTAC---TACTATGACCAAAATTTCCGGAATCA 401  
Db 123 ThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeuPheGln 142  
QY 402 TGCCGCCCATGTACCAAGTGTCCCAAGGAATCCCTGCTCCTCCAGGAATCAACTCCACA 461  
Db 143 CysPheAsnCysSerLeuCysLeuAsnGly---ThrValHisLeuSerCysGlnGluLys 161  
QY 462 GCTAACACTGTGTGCACTTCA-----TCT 485  
Db 162 GlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSer 181  
QY 486 GTTTCAAATCCCAAGAACTGGCTGTCTACTGATGCTAAATGTCTTCTGATCTGAAGA 545  
Db 182 CysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIle-GluAs 201  
QY 546 AGATAAGGTTCTACAGATGGTGTCTGATGCTCCTTCTTCTTTATGCTG 591  
Db 201 nValLysGlyThrGluAspSerGlyThrValLeuLeuProLeu 216

## RESULT 11

US-08-837-941-2  
; Sequence 2, Application US/08837941  
; Patent No. 5766917  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BRAKEBUSCH, Cord  
; APPLICANT: VARFOLOMEEV, Eugene  
; APPLICANT: BATKIN, Michael  
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,941  
; FILING DATE: 28-APR-1997  
; CLASSIFICATION: 435



QY 171 CCTCAGGTACATTTGTCAGGCGCCCTGCAAAATCCCCATCTACTCAAGACATGTGAG 230  
Db 63 H1sLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArg 82  
QY 231 AAGTGTCCAGCAGACATTCACAGGAAAGATAATGGCTGCATGATTGTGAACCTTGC 290  
Db 83 GluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgH1sCysLeuSerCys 102  
QY 291 TCCACCTGTGATAAAGCAGACATATGGTG-----GCTGACTGTGTTCTGCCACCAAGTGC 344  
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QY 345 CGAAATGCGAGTGCCTCAATAGTCTTTAC---TACTATGACCCCAAAATTTCCGGATCA 401  
Db 123 ThrValCysGlyThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSer 181  
QY 486 GTTTCAAATCCAGAACTGGGTGTTCTCCTACTGATGCTAATGTCTTCTGTATCTGAAGA 545  
Db 182 CysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIle-GluAs 201  
QY 546 AGATAAGGTCTTACAGATGGTGTCTGAGTCTTCTTCTTATTGCTG 591  
Db 201 nValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeu 216

## RESULT 13

US-08-465-982-25  
; Sequence 25, Application US/08465982  
; Patent No. 5863786  
; GENERAL INFORMATION:  
; APPLICANT: M. Feldmann, P.W. Gray,  
; APPLICANT: M.J.C. Turner, F.M. Brennan  
; TITLE OF INVENTION: Modified human TNFalpha (Tumor  
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robbins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,982  
; FILING DATE:  
; CLASSIFICATION:

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/050,319  
; FILING DATE: 10-May-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robbins, Roberta L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 5150-0030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 617-8999  
; TELEFAX: (415) 327-3231  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-465-982-25

## Alignment Scores:

Pred. No.: 6,15e-15 Length: 455  
Score: 207.50 Matches: 65  
Percent Similarity: 42.13% Conservative: 26  
Best Local Similarity: 30.09% Mismatches: 95  
Query Match: 7.67% Indels: 30  
DB: 2 Gaps: 7

US-09-855-266A-3 (1-1509) x US-08-465-982-25 (1-455)

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QY 84 -----CCGGTAATATTGCTATGCT-----GAATCATCTACTCCTTC 119  
Db 23 TyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArgAspSer 42  
QY 120 AACTGTCCGATGGTGAATAC-----CAGTCTAATGATGCTGTGTGCAAGACCTGT 170  
Db 43 ValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThrLysCys 62  
QY 171 CCCTCAGTACATTTGTCAAGCGCCCTGCAAAATCCCCATCTACTCAAGGACAAATGTGAG 230  
Db 63 H1sLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArg 82  
QY 231 AAGTGTACCCAGGACATTCACAGGAAAGATAATGCTGCTGATGTTGAACCTTGC 290  
Db 83 GluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeuSerCys 102  
QY 291 TCCACCTGTGATAAAGACAGATATGTG-----GCTGACTGTGTTCTGCCACCAAGTGC 344  
Db 103 SerLysCysArgLysGluMetGlyGlnValGluLeuSerSerCysThrValAspArgAsp 122  
QY 345 CGAAATGCGAGTGCCTCAATAGTCTTTAC---TACTATGACCCCAAAATTTCCGGATCA 401  
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QY 402 TCCGCCCCATGTACCAAGTGTCCCCAAGAAATCCCTGCTCCAGGAATGCAACATCCACA 461  
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QY 462 GCTAACACTGTGTGCAGTTCA-----TCT 485  
Db 162 GlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSer 181  
QY 486 GTTTCAAATCCAGAACTGGCTGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 545  
Db 182 CysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIle-GluAs 201  
QY 546 AGATAAAGGTCTTACAGATGGTGTGCTGAGTCTTCTTCTTATTGCTG 591  
Db 201 nValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeu 216

## RESULT 14

US-08-465-982-25  
; Sequence 5, Application US/08815469  
; Patent No. 6153402  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Genitz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington

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123 ThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeuPheGln 142
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QY 462 GCTAACACTGTGTGCAGTTCA-----TCT 485
Db 162 GlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSer 181
QY 486 GTTTCAAATCCCAAGAACTGGCTGTTCTCTACTGATGCTAAATTGCTTCTGTATCTGAAGA 545
Db 182 CysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIle-GluAs 201
QY 546 AGATAAAGTGTACAGATGGTGTCTAGCTTCCCTTTTATTGTGTG 591
Db 201 nValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeu 216

RESULT 15
US-09-006-353A-3
; Sequence 3, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006.353A
; FILING DATE:

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83	GluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeuSerCys	102		
291	TCCACCTGTGATAAAGACCAAGATATGGTG	-----GCTGACTGTTCTGCCACCACTGAC	344	
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-006-353A-3

Alignment Scores:
Pred. No.: 6,15e-15
Score: 207.50
Percent Similarity: 42.13%
Best Local Similarity: 30.09%
Query Match: 7.67%
DB: 3

Length: 455
Matches: 65
Conservative: 26
Mismatches: 95
Indels: 30
Gaps: 7

US-09-855-266A-3 (1-1509) x US-09-006-353A-3 (1-455)

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+ + + + +
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QY      120 AACTGTCGGATGGTGAATAC-----CAGTCTAATGATGCTGTGTGCAAGACCTGT 170
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QY      171 CCCTCAGGTACATTGCTCAAGCGCCCTGCAAAATCCCCATACTCAAGGACAAATGTGAG 230
Db      63 HisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArg 82
QY      231 AAGTGTCAACCCAGGACATTCACAGGGAAGATAATGGCTGCATGATTGTGAACCTTGC 290
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Db      143 CysPheAsnCysSerLeuCysLeuAsnGly---ThrValHisLeuSerCysGlnGluLys 161
QY      462 GCTAACACTGTGTGCAGTTCA-----TCT 485
Db      162 GlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSer 181
QY      486 GTTTCAAATCCAGAACTGGCTGTCTCTACTCATGCTAATGCTCTCTCTATCTCAAGA 545
Db      182 CysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIle-GluAs 201
QY      546 AGATAAAGTTCTACAGATGGTGTCTGTAGTTCCTTTTATTGCTG 591
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Job time : 32.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 20, 2003, 13:34:53 ; Search time 66 Seconds  
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6034.249 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 497079 seqs, 131961718 residues

Total number of hits satisfying chosen parameters: 994158

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database : Published Applications\_AA.\*

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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
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1	1000	37.0	176	10	US-09-855-266A-1	Sequence 1, Appl1
2	1000	37.0	176	15	US-10-193-616-8	Sequence 8, Appl1
3	917	33.9	396	15	US-10-193-616-14	Sequence 14, Appl1
4	858	31.7	148	10	US-09-855-266A-2	Sequence 2, Appl1
5	668	24.7	117	15	US-10-193-616-6	Sequence 6, Appl1
6	216.5	8.0	461	9	US-09-899-422-15	Sequence 15, Appl1
7	216.5	8.0	461	10	US-09-898-234-15	Sequence 15, Appl1
8	216.5	8.0	461	10	US-09-899-429A-25	Sequence 25, Appl1
9	216.5	8.0	461	10	US-09-792-356-15	Sequence 15, Appl1
10	215.5	8.0	247	15	US-10-193-616-10	Sequence 10, Appl1
11	213.5	7.9	162	9	US-09-798-789-13	Sequence 13, Appl1
12	213.5	7.9	162	16	US-10-218-102-423	Sequence 423, App
13	212.5	7.9	123	10	US-09-855-266A-13	Sequence 13, Appl1
14	207.5	7.7	162	9	US-09-798-789-15	Sequence 15, Appl1
15	207.5	7.7	162	16	US-10-218-102-425	Sequence 425, App
16	207.5	7.7	371	9	US-09-899-422-12	Sequence 12, Appl1
17	207.5	7.7	371	10	US-09-898-234-12	Sequence 12, Appl1
18	207.5	7.7	371	10	US-09-792-356-12	Sequence 12, Appl1
19	207.5	7.7	455	9	US-09-826-212-3	Sequence 3, Appl1
20	207.5	7.7	455	9	US-09-333-966-5	Sequence 5, Appl1
21	207.5	7.7	455	9	US-09-027-287-3	Sequence 3, Appl1
22	207.5	7.7	455	9	US-09-874-138-3	Sequence 3, Appl1
23	207.5	7.7	455	9	US-09-840-707A-16	Sequence 16, Appl1
24	207.5	7.7	455	9	US-09-252-656B-3	Sequence 3, Appl1
25	207.5	7.7	455	9	US-09-899-422-2	Sequence 2, Appl1
26	207.5	7.7	455	9	US-09-899-422-17	Sequence 17, Appl1
27	207.5	7.7	455	10	US-09-935-727-5	Sequence 5, Appl1
28	207.5	7.7	455	10	US-09-898-234-2	Sequence 2, Appl1
29	207.5	7.7	455	10	US-09-898-234-17	Sequence 17, Appl1
30	207.5	7.7	455	10	US-09-756-854-5	Sequence 5, Appl1
31	207.5	7.7	455	10	US-09-899-429A-2	Sequence 2, Appl1
32	207.5	7.7	455	10	US-09-899-429A-27	Sequence 27, Appl1
33	207.5	7.7	455	10	US-09-792-356-2	Sequence 2, Appl1
34	207.5	7.7	455	10	US-09-792-356-17	Sequence 17, Appl1
35	207.5	7.7	455	11	US-09-314-889-5	Sequence 5, Appl1
36	207.5	7.7	455	13	US-10-005-842-3	Sequence 3, Appl1
37	207.5	7.7	455	14	US-10-120-397-2	Sequence 2, Appl1
38	207.5	7.7	455	14	US-10-041-574-5	Sequence 5, Appl1
39	207.5	7.7	455	15	US-10-252-408-4	Sequence 4, Appl1
40	207.5	7.7	455	15	US-10-038-557A-16	Sequence 16, Appl1
41	207.5	7.7	455	15	US-10-175-902-4	Sequence 4, Appl1
42	207.5	7.7	455	15	US-10-186-643-3	Sequence 3, Appl1
43	206.5	7.6	355	9	US-09-826-212-14	Sequence 14, Appl1
44	206.5	7.6	355	10	US-09-935-727-16	Sequence 16, Appl1
45	206.5	7.6	355	15	US-10-186-643-14	Sequence 14, Appl1

ALIGNMENTS

RESULT 1

; Sequence 1, Application US/09855266A  
; Patent No. US20020128435A1  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501-040002  
; CURRENT APPLICATION NUMBER: US/09/855,266A  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR FILING DATE: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-855-266A-1

Score:	1000.00	Matches:	176
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	36.98%	Indels:	0
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US-09-855-266A-3 (1-1509) x US-10-193-616-8 (1-176)

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DB	21	AsnLeuPheLeuProValIlePheAlaMetProGluSerTyrSerPheAsnCysProAsp	40
QY	132	GGTGAATACCAAGTCTAATCATGCTGTGTTCAAGACCTGTCCCTCAGGTACATTTGTCAAG	19
DB	41	GlyGluTyrGlnSerAsnAspValCysCysLysThrCysProSerGlyThrPheValLys	60
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DB	61	AlaProCysLysIleProHisThrGlnGlnGlnCysGluLysCysHisProGlyThrPhe	80
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DB	101	AsnMetValAlaAspCysSerAlaThrSerAspArgLysCysGluCysGlnIleGlyLeu	12
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DB	141	IleProValLeuGlnGluCysAsnSerThrAlaAsnThrValCysSerSerValSer	16
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RESULT 3

US-10-193-616-14

; Sequence 14, Application US/10193616

; Publication No. US20030096355A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Ke

; TITLE OF INVENTION: Isolation, Identification, and Characterization of ymkz5, a novel

; TITLE OF INVENTION: ymkz5, a novel

; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family

; FILE REFERENCE: 01017/35551A

; CURRENT APPLICATION NUMBER: US/10/193,616

; CURRENT FILING DATE: 2002-07-11

; PRIOR APPLICATION NUMBER: US/09/611,989

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,137

; PRIOR FILING DATE: 1999-07-07

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 396

; TYPE: PRT

; ORGANISM: Mus musculus

; FEATURE:

; OTHER INFORMATION: ymkz5-Fc fusion protein

US-10-193-616-14

Alignment Scores:	3.82e-83	Length:	396
Pred. No.:	917.00	Matches:	161

Score:

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 33.91%  
DB: 15  
Indels: 0  
Gaps: 0

US-09-855-266A-3 (1-1509) x US-10-193-616-14 (1-396)

QY 12 ATGGTTACCTTCAGCCACGCTCTCCAGTCTGAGTCACTGGTTCCTCTGCTGCTGCTG 71  
DB 1 MetValThrPheSerHisValSerSerLeuSerHisTrpPheLeuLeuLeuLeuLeu 20  
QY 72 AATCTGTTCTGCGGTAAATATTTGTATGCTGTAATCATACCTTCCTCACTGTCCTGAT 131  
DB 21 AsnLeuPheLeuProValIlePheAlaMetProGluSerTyrrSerPheAsnCysProAsp 40  
QY 132 GGTGAATACCACTTAATGATGCTCTTGCACAGACCTGTCCTTCAGGTACATTTGTCAAG 191  
DB 41 GlyGluTyrrGlnSerAsnAspValCysLysLysLysLysLysLysLysLysLysLys 60  
QY 192 GCGCCCTGCAAAATCCCCATCTCAAGGACAAATGTGAGAAAGTGTACCCAGGAACATTC 251  
DB 61 AlaProCysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 80  
QY 252 ACAGGAAAGATAATGGCTGCTGATGATGTGAATCTTGTCCACCTGTGTGATAAGACCAG 311  
DB 81 ThrGlyLysAspAsnGlyLeuHisAspCysGluLeuCysSerThrCysAspLysAspGln 100  
QY 312 AATATGGTGGCTGACTGTTCTGCCACCACTGACCGAAGTGTACCGAAGTGTCCCAAGTCTT 371  
DB 101 AsnMetValAlaAspCysSerAlaThrSerAspArgLysCysGluCysGluCysGlu 120  
QY 372 TACTACTATGACCCAAATTTCCGGAATCATGCCGCCATGTACCAAGTGTCCCAAGGA 431  
DB 121 TyrTyrrAspProLysPheProGluSerCysArgProCysThrLysCysProGlnGly 140  
QY 432 ATCCCTGCTCCTCAGGAAGTCAACTCCACAGCTAACACTGTGTGCACTGTTCACTGTGTTCA 491  
DB 141 IleProValLeuGlnGluCysAsnSerThrAlaAsnThrValCysSerSerValSer 160  
QY 492 AAT 494  
DB 161 Asn 161

RESULT 4

US-09-855-266A-2  
; Sequence 2, Application US/09855266A  
; Patent No. US20020128435A1  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501-040002  
; CURRENT APPLICATION NUMBER: US/09/855,266A  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 09/411,722  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-855-266A-2

Alignment Scores:  
Pred. No.: 2.39e-77 Length: 148  
Score: 858.00 Matches: 148  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0

Query Match: 31.73%  
DB: 10  
Indels: 0  
Gaps: 0  
US-09-855-266A-3 (1-1509) x US-09-855-266A-2 (1-148)

QY 96 GCTATGCTGAATCATACTCTTCAACAGTGTCCGATGTCCGATGAATACCACTCTAATGATGTC 155  
DB 1 AlaMetProGluSerTyrrSerPheAsnCysProAspGlyGluTyrrGlnSerAsnAspVal 20  
QY 156 TGTTCGAAGACCTGCTCCTCAGGTACATTTTGTCAAGGCGCCCTGCAAAATCCCATACT 215  
DB 21 CysCysLysThrCysProSerGlyThrPheValLysAlaProCysLysLysLysLysLys 40  
QY 216 CAAGGACAAATGTGAGAAGTGTCCACCGAGAAATTCACAGGAGAAAGATAATGGCTGCTGAT 275  
DB 41 GlnGlyGlnCysGluLysCysHisProGlyThrPheThrGlyLysAspAsnGlyLeuHis 60  
QY 276 GATTGTGAACCTTGTCTCCACCTGTGATAAAGACCAAGATAATGGTGGCTGACTGTTCTGCC 335  
DB 61 AspCysGluLeuCysSerThrCysAspLysAspGlnAsnMetValAlaAspCysSerAla 80  
QY 336 ACCAGTGACCCGAAATGCGAGTGTCCCAAGTGTCCCAAGGAAATCCCTGTCTCCAGGAATGCAAC 395  
DB 81 ThrSerAspArgLysCysGluCysGlnIleGlyLeuTyrrTyrrAspProLysPhePro 100  
QY 396 GAATCATGCCGCCATGTACCAAGTGTCCCAAGGAAATCCCTGTCTCCAGGAATGCAAC 455  
DB 101 GluSerCysArgProCysThrLysCysProGlnGlyIleProValLeuGlnGluCysAsn 120  
QY 456 TCCACAGCTAACACTGTGTGCACTGTCTCTTCAAAATCCAGAAATGCTGCTGTTCTCTA 515  
DB 121 SerThrAlaAsnThrValCysSerSerValSerAsnProArgAsnTrpLeuPheLeu 140  
QY 516 CTGATGCTAATGCTCTCTCTGATC 539  
DB 141 LeuMetLeuIleValPheCysIle 148

RESULT 5

US-10-193-616-6  
; Sequence 6, Application US/10193616  
; Publication No. US20030096355A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ke  
; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
; TITLE OF INVENTION: ymkz5, a novel  
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family  
; FILE REFERENCE: 01017/35551A  
; CURRENT APPLICATION NUMBER: US/10/193,616  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: US/09/611,989  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,137  
; PRIOR FILING DATE: 1999-07-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-193-616-6

Alignment Scores:  
Pred. No.: 2.65e-58 Length: 117  
Score: 668.00 Matches: 117  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Query Match: 24.70%  
DB: 15  
Indels: 0  
Gaps: 0

US-09-855-266A-3 (1-1509) x US-10-193-616-6 (1-117)

QY 12 ATGGTTACCTTCAGCCACGCTCTCCAGTGTGCTGATGCTGTTCTCTGCTGCTGCTG 71  
|||||



Db 1 MetValThrPheSerHisValSerSerLeuSerHisTrpPheLeuLeuLeuLeuLeuLeu 20  
QY 72 AATCTGTTGTCGCGGTAATTTGCTATGCTGAATCATACTCTTCAACTGTCCCGAT 131  
Db 21 AsnLeuPheLeuProValIlePheAlaMetProGluSerTyrSerPheAsnCysProAsp 40  
QY 132 GGTCAATACCACTAATGATGCTGTTCAGACCTGCTCCCTCAGGTACATTTCCTCAAG 191  
Db 41 GlyGluTyrGlnSerAsnAspValCysCysLysThrCysProSerGlyThrPheValLys 60  
QY 192 GCGCCCTGCAAAATCCCCATPACTCAAGGACAATGTGAGAAGTGTCCACCCAGGAACATTC 251  
Db 61 AlaProCysLysIleProHisThrGlnGlyGlnCysGluLysCysHisProGlyThrPhe 80  
QY 252 ACAGGAAAGATATGCGCTGCATGATGTAATTTGCTCCACTGCTGATAAAGACAG 311  
Db 81 ThrGlyLysAspAsnGlyLeuHisAspCysGluLeuCysSerThrCysAspLysAspGln 100  
QY 312 AATATGTTGGCTGACTGTTCTGCCACCACTGACCGGAATGCGAGTGCCTCA 362  
Db 101 AsnMetValAlaAspCysSerAlaThrSerAspArgLysCysGluCysGln 117

## RESULT 6

US-09-899-422-15  
; Sequence 15, Application US/09899422  
; Patent No. US2002090676A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; FILE REFERENCE: 98,385-H  
; CURRENT APPLICATION NUMBER: US/09/899,422  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8

US-09-899-422-15

Alignment Scores:  
Pred. No.: 8.56e-13 Length: 461  
Score: 216.50 Matches: 63  
Percent Similarity: 39.45% Conservative: 23  
Best Local Similarity: 28.90% Mismatches: 71  
Query Match: 8.01% Indels: 61  
DB: 9 Gaps: 9

US-09-855-266A-3 (1-1509) x US-09-899-422-15 (1-461)

QY 123 TGTCGCCGATGTAATAC-----CAGTCTAATGATGCTGTGTGCAAGACCTGCTCC 173  
Db 44 CysProGlnGlyLysTyrAlaHisProLysAsnAsnSerIleCysCysThrLysCysHis 63  
QY 174 TCAGGTACATTTGCAAGCGCCCTGCAAAATCCCCATACATCAAGGACAAATGTGAGAG 233  
Db 64 LysGlyThrTyrLeuValSerAspCysProSerProGlyGlnGluThrValCysGluLeu 83

QY 234 TGTCAACCCAGGAACATTCACAGGAAGAATAATGGCTGCGATGATTGTGAACTTTCTCTCC 293  
Db 84 SerHisLysGlyThrPheThrAlaSerGlnAsnHisValArgGlnCysLeuSerCysLys 103  
QY 294 ACCTGTGATAAGAC-----CAGATATATGGTGGCTGACTGTTCTCCACCACTGACCGG 347  
Db 104 ThrCysArgLysGluMetPheGlnValGluIleSerProCysLysAlaAspMetAspThr 123  
QY 348 AATCGAGTGC-----CAATATAGGTCTTTTACTACTATGACCCAAAATTTCCGGAA 398  
Db 124 ValCysGlyCysLysLysAsnGlnPheGlnArgTyrLeuSerGluThrHisPhe----- 141  
QY 399 TCATGCCGCCCATGTACCAAGTGTCCCAAGGA-----ATCCCTGTCTCTCCAGGAA 449  
Db 142 GlnCysValAspCysSerProCysPheAsnGlyThrValThrIleProCysLysGluLys 161  
QY 450 TCAACTCCACAGCTAAC-----ACTGTG 473  
Db 162 GlnAsnThrValCysAsnCysHisAlaGlyPhePheLeuSerGlyAsnGluCysThrPro 181  
QY 474 TGCAGTTTCATCTGTTTCAAAATCCAG-----AAACTGGCTGTCTCTACTGATGCTA 524  
Db 182 CysSer-His-CysLysLysAsnGlnGluCysMetLysLeuCysLeuProValAla 201  
QY 525 AT----- 526  
Db 201 snValThrAsnProGlnAspSerGlyThrAlaValLeuLeuProLeuValIlePheLeuG 221  
QY 527 -----TGCTCTCTGATATCTGAAGAAGATAAGGTTCTACAGATGGTCTGTAGCTTCT 581  
Db 221 lylLeuLeuLeuPhePheIleCysIleSerLeuLeu----- 233  
QY 582 TTTATTGCTGTGAAGAGAAACCATGGAGGCAACTCTTTCATTTATTTA 631  
Db 234 -----CysArgTyrProGlnTrpArgProArgValTyrSerIle 247

## RESULT 7

US-09-898-234-15  
; Sequence 15, Application US/09898234  
; Patent No. US20020155112A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; FILE REFERENCE: 98,385-1  
; CURRENT APPLICATION NUMBER: US/09/898,234  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8

US-09-898-234-15

Alignment Scores:

Pred. No.: 8.56e-13 Length: 461

Score: 216.50 Matches: 63  
Percent Similarity: 39.45% Conservative: 23  
Best Local Similarity: 28.90% Mismatches: 71  
Query Match: 8.01% Indels: 61  
DB: 10 Gaps: 9

US-09-855-266A-3 (1-1509) x US-09-899-234-15 (1-461)

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QY 123 TGTCCCGATGGTGAATAC-----CAGTCTAATGATGCTGTGTTGCAAGACCTGTGCC 173
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 44 CysProGlnGlyLysTyrAlaHisProLysAsnAsnSerIleCysCysThrLysCysHis 63

QY 174 TCAGGTACATTTGTCAAGCGCCCTGCAAAATCCCCATCTCAAGACAATGTGAGAAG 233
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 LysGlyThrTyrLeuValSerAspCysProSerProGlyGlnGluThrValCysGluLeu 83

QY 234 TGTCAACCCAGGACATTCACAGGAAGATAAATGGCTGCATGATGCTGACITTTGCTCC 293
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 84 SerHisLysGlyThrPheThrAlaSerGlnAsnHisValArgGlnCysLysLeuSerCysLys 103

QY 294 ACCTGTGATAAAGAC-----CAGAAATATGCTGGCTGACTGTTCTGCCACAGTGACCGG 347
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 104 ThrCysArgLysGluMetPheGlnValGluIleSerProCysLysAlaAspMetAspThr 123

QY 348 AAATCGAGTGC-----CAAATAGCTTTTACTACTATGACCCCAAAATTTCCGGAA 398
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 124 ValCysGlyCysLysLysAsnGlnPheGlnArgTyrLeuSerGluThrHisPhe----- 141

QY 399 TCATGCGGCCCATGTACCAAGTGTCCCAAGGA-----ATCCCTGTCTCCAGGAA 449
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 142 GlnCysValAspCysSerProCysPheAsnGlyThrValThrIleProCysLysGluLys 161

QY 450 TGCAACTCCACAGCTAAC-----CAATAGTCTTTTACTACTATGACCCCAAAATTTCCGG 473
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 162 GlnAsnThrValCysAsnCysHisAlaGlyPhePheLeuSerGlyAsnGluCysThrPro 181

QY 474 TGCAGTCTATCTGTTTCAAATCCCAG-----AAACTGGCTGTCTCTACTGATGCTA 524
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 CysSer-His-CysLysLysAsnGlnGluCysMetLysLeuCysLeuProProValAlaA 201

QY 525 AT----- 526
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 201 snValThrAsnProGlnAspSerGlyThrAlaValLeuLeuProLeuValIlePheLeuG 221

QY 527 -----TGTCTTCTGTATCTGAAGAGATAAAGTCTTACAGATGGTGTCTGTAGTTCCT 581
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 221 LysLeuCysLeuLeuPhePheIleCysIleSerLeuLeu----- 233

QY 582 TTTATTGCTGTGAAGAGAAACCATGGAGCAACTCTTTCATTTATTTT 631
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 234 -----CysArgTyrProGlnTyrArgProArgProArgValTyrSerIleIle 247
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## RESULT 8

US-09-899-429A-25  
; Sequence 25, Application US/09899429A  
; Patent No. US20020169118A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; TITLE OF INVENTION: Them  
; FILE REFERENCE: 98-385-J  
; CURRENT APPLICATION NUMBER: US/09/899,429A  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/792,356  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 08/477,639  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287

; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 25  
; TYPE: PRT  
; LENGTH: 461  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8  
US-09-899-429A-25

## Alignment Scores:

Pred. No.: 8,566-13 Length: 461  
Score: 216.50 Matches: 63  
Percent Similarity: 39.45% Conservative: 23  
Best Local Similarity: 28.90% Mismatches: 71  
Query Match: 8.01% Indels: 61  
DB: 10 Gaps: 9

US-09-855-266A-3 (1-1509) x US-09-899-429A-25 (1-461)

```
QY 123 TGTCCCGATGGTGAATAC-----CAGTCTAATGATGCTGTGTTGCAAGACCTGTGCC 173
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 44 CysProGlnGlyLysTyrAlaHisProLysAsnAsnSerIleCysCysThrLysCysHis 63

QY 174 TCAGGTACATTTGTCAAGCGCCCTGCAAAATCCCCATCTCAAGACAATGTGAGAAG 233
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 LysGlyThrTyrLeuValSerAspCysProSerProGlyGlnGluThrValCysGluLeu 83

QY 234 TGTCAACCCAGGACATTCACAGGAAGATAAATGGCTGCATGATGCTGACITTTGCTCC 293
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 84 SerHisLysGlyThrPheThrAlaSerGlnAsnHisValArgGlnCysLysLeuSerCysLys 103

QY 294 ACCTGTGATAAAGAC-----CAGAAATATGCTGGCTGACTGTTCTGCCACAGTGACCGG 347
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 104 ThrCysArgLysGluMetPheGlnValGluIleSerProCysLysAlaAspMetAspThr 123

QY 348 AAATCGAGTGC-----CAAATAGTCTTTTACTACTATGACCCCAAAATTTCCGGAA 398
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 124 ValCysGlyCysLysLysAsnGlnPheGlnArgTyrLeuSerGluThrHisPhe----- 141

QY 399 TCATGCGGCCCATGTACCAAGTGTCCCAAGGA-----ATCCCTGTCTCCAGGAA 449
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 142 GlnCysValAspCysSerProCysPheAsnGlyThrValThrIleProCysLysGluLys 161

QY 450 TGCAACTCCACAGCTAAC-----CAATAGTCTTTTACTACTATGACCCCAAAATTTCCGG 473
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 162 GlnAsnThrValCysAsnCysHisAlaGlyPhePheLeuSerGlyAsnGluCysThrPro 181

QY 474 TGCAGTCTATCTGTTTCAAATCCCAG-----AAACTGGCTGTCTCTACTGATGCTA 524
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 CysSer-His-CysLysLysAsnGlnGluCysMetLysLeuCysLeuProProValAlaA 201

QY 525 AT----- 526
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 201 snValThrAsnProGlnAspSerGlyThrAlaValLeuLeuProLeuValIlePheLeuG 221

QY 527 -----TGTCTTCTGTATCTGAAGAGATAAAGTCTTACAGATGGTGTCTGTAGTTCCT 581
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 221 LysLeuCysLeuLeuPhePheIleCysIleSerLeuLeu----- 233

QY 582 TTTATTGCTGTGAAGAGAAACCATGGAGCAACTCTTTCATTTATTTT 631
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 234 -----CysArgTyrProGlnTyrArgProArgProArgValTyrSerIleIle 247
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## RESULT 9

US-09-792-356-15  
; Sequence 15, Application US/09792356  
; Publication No. US20020183485A1

GENERAL INFORMATION:  
 APPLICANT: Hauptmann, Rudolph  
 APPLICANT: Himmler, Adolph  
 APPLICANT: Maurer-Fogy, Ingrid  
 APPLICANT: Stratowa, Christian  
 TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 TITLE OF INVENTION: Them  
 FILE REFERENCE: 98,385-G  
 CURRENT APPLICATION NUMBER: US/09/792,356  
 CURRENT FILING DATE: 2001-08-17  
 PRIOR APPLICATION NUMBER: 08/477,639  
 PRIOR FILING DATE: 1995-06-07  
 PRIOR APPLICATION NUMBER: 08/383,676  
 PRIOR FILING DATE: 1995-02-01  
 PRIOR APPLICATION NUMBER: 08/153,287  
 PRIOR FILING DATE: 1993-11-17  
 PRIOR APPLICATION NUMBER: 07/821,750  
 PRIOR FILING DATE: 1992-01-02  
 PRIOR APPLICATION NUMBER: 07/511,430  
 PRIOR FILING DATE: 1990-04-20  
 NUMBER OF SEQ ID NOS: 87  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 15  
 LENGTH: 461  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8  
 US-09-792-356-15

Alignment Scores:  
 Pred. No.: 8,566-13 Length: 461  
 Score: 216.50 Matches: 63  
 Percent Similarity: 39.45% Conservative: 23  
 Best Local Similarity: 28.90% Mismatches: 71  
 Query Match: 8.01% Indels: 61  
 DB: 10 Gaps: 9

US-09-855-266A-3 (1-1509) x US-09-792-356-15 (1-461)

Qy 123 TGTCCCGATGTTGAATAC-----CAGTCTAATGATGCTGTTCGCAAGACCTGTCC 173  
 Db 44 CysProGlnGlyLysTyrValHisProLysAsnAsnSerIleCysCysThrLysCysHis 63  
 Qy 174 TCAGTACATTTGTCAAGCGCCCTGCAAAATCCCCATCTACTACAGGCAATGTGAGAAG 233  
 Db 64 LysGlyThrTyrLeuValSerAspCysProSerProGlyGlnGluThrValCysGluLeu 83  
 Qy 234 TGTACCCAGGACATTCACAGGGAAGATATGGCTGCATGATGTGAACCTTGTCTCC 293  
 Db 84 SerHisLysGlyThrPheThrAlaSerGlnAsnHisValArgGlnCysLeuSerCysLys 103  
 Qy 294 ACCTGTGATAAGAC-----CAGAATATGGTGGCTGACTGTTCTGCCACCACTGACCGG 347  
 Db 104 ThrCysArgLysGluMetPheGlnValGluIleSerProCysLysAlaAspMetAspThr 123  
 Qy 348 AAATCGAGTGC-----CAAAATAGTCTTACTATGACCCCAAAATTTCCGGAA 398  
 Db 124 ValCysGlyCysLysLysAsnGlnPheGlnArgTyrLeuSerGluThrHisPhe----- 141  
 Qy 399 TCATCGCGCCCATGATACCAAGTGTCCCAAGGA-----ATCCCTGTCTCCAGGAA 449  
 Db 142 GlnCysValAspCysSerProCysPheAsnGlyThrValThrIleProCysLysGluLys 161  
 Qy 450 TGCRACTCACAGCTAAC-----ACTGTG 473  
 Db 162 GlnAsnThrValCysAsnCysHisAlaGlyPheLeuSerGlyAsnGluCysThrPro 181  
 Qy 474 TGCAGTTCATCTGTTTCAATCCAG-----AACTGGCTGTCTTCTACTGATGCTTA 524  
 Db 182 CysSer-His-CysLysLysAsnGlnGluCysMetLysLeuCysLeuProProValAla 201  
 Qy 525 AT----- 526

Db 201 snValThrAsnProGlnAspSerGlyThrAlaValLeuLeuProLeuValIlePheLeuG 221  
 Qy 527 -----TGTCTTCTGTATCTGAAGAAGATAAGGTTCTACAGATGGTCTGTAGCTTCCT 581  
 Db 221 LysCysLeuLeuPhePheIleCysIleSerLeuLeu----- 233  
 Qy 582 TTTATTGCTGTGAAGAGAAACCATGGAGGCAACTCTTTCAATTTATTTT 631  
 Db 234 -----CysArgTyrProGlnTrpArgProArgValTyrSerIleIle 247

RESULT 10  
 US-10-193-616-10  
 ; Sequence 10, Application US/10193616  
 ; Publication No. US2003009635A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Ke  
 ; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
 ; TITLE OF INVENTION: ymkz5, a novel  
 ; FILE REFERENCE: 01017/3551A  
 ; CURRENT APPLICATION NUMBER: US/10/193,616  
 ; CURRENT FILING DATE: 2002-07-11  
 ; PRIOR APPLICATION NUMBER: US/09/611,989  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/143,137  
 ; PRIOR FILING DATE: 1999-07-07  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; OTHER INFORMATION: TNFRI  
 US-10-193-616-10

Alignment Scores:  
 Pred. No.: 8,956-13 Length: 247  
 Score: 215.50 Matches: 52  
 Percent Similarity: 40.54% Conservative: 23  
 Best Local Similarity: 28.11% Mismatches: 61  
 Query Match: 7.97% Indels: 49  
 DB: 15 Gaps: 7

US-09-855-266A-3 (1-1509) x US-10-193-616-10 (1-247)

Qy 123 TGTCCCGATGTTGAATAC-----CAGTCTAATGATGCTGTTCGCAAGACCTGTCC 173  
 Db 44 CysProGlnGlyLysTyrValHisSerLysAsnAsnSerIleCysCysThrLysCysHis 63  
 Qy 174 TCAGTACATTTGTCAAGCGCCCTGCAAAATCCCCATCTACTACAGGCAATGTGAGAAG 233  
 Db 64 LysGlyThrTyrLeuValSerAspCysProSerProGlyArgAspThrValCysArgGlu 83  
 Qy 234 TGTACCCAGGACATTCACAGGGAAGATATGGCTGCATGATGTGAACCTTGTCTCC 293  
 Db 84 CysGluLysGlyThrPheThrAlaSerGlnAsnTyrLeuArgGlnCysLeuSerCysLys 103  
 Qy 294 ACCTGTGATAAGACCAAGATATGGTG-----GCTGACTGTTCTGCCACCACTGACCGG 347  
 Db 104 ThrCysArgLysGluMetSerGlnValGluIleSerProCysGlnAlaAspLysAspThr 123  
 Qy 348 AAATCGAGTGC-----CAAAATAGTCTTACTATGACCCCAAAATTTCCGGAA 398  
 Db 124 ValCysGlyCysLysGluAsnGlnPheGlnArgTyrLeuSerGluThrHisPhe----- 141  
 Qy 399 TCATCGCGCCCATGATACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAAATCAACTCC 458  
 Db 142 GlnCysValAspCysSerProCysPheAsnGly---ThrValThrIleProCysLysGlu 160  
 Qy 459 ACAGTAAACACTGTGTGCACT----- 479

Db 161 ThrGlnAsnThrValCysAsnCysHisAlaGlyPhePheLeuArgGluSerGluCysVal 180  
QY 479 -----  
Db 181 ProCysSerHisCysLysLysAsnGluGluCysMetLysLeuCysLeuProProLeu 200  
QY 480 TCATCTGTTTCAAAATCCAGAAC-----TGGCTGTTCTTACTGATGCTA 524  
Db 201 AlaAsnValThrAsnProGlnAspSerGlyThrAlaValLeuLeuProLeuValIleLeu 220  
QY 525 ATTGTCTTCTGATC 539  
Db 221 LeuGlyLeuCysLeu 225

## RESULT 11

US-09-798-789-13  
; Sequence 13, Application US/09798789  
; Patent No. US20020009780A1  
; GENERAL INFORMATION:  
; APPLICANT: Dahiyat, Basil  
; APPLICANT: Fillikov, Anton  
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA  
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED  
; TITLE OF INVENTION: DISORDERS  
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/09/798,789  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: US 60/186,427  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-798-789-13

Alignment Scores:  
Pred. No.: 1,25e-12 Length: 162  
Score: 213.50 Matches: 44  
Percent Similarity: 47.20% Conservative: 15  
Best Local Similarity: 35.20% Mismatches: 59  
Query Match: 7.90% Indels: 7  
DB: 9 Gaps: 4

US-09-855-266A-3 (1-1509) x US-09-798-789-13 (1-162)

QY 123 TGTCCCGATGGTGAATAC-----CAGTCTAATGATGTCGTGCAAGACCTGTGCC 173  
Db 5 CysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThrLysCysHis 24  
QY 174 TCAGGTACATTGTCAAGCGCCCTGCAAAATCCCATACTCAAGGACAAATGTGAGAAG 233  
Db 25 LysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGlu 44  
QY 234 TGTCAACCCAGGAACATTCACAGGGAAGATATGCGCTGCATGATGTTGAATTTGCTCC 293  
Db 45 CysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgAspCysLeuGlnCysSer 64  
QY 294 ACCTGTGATAAGACCAAGATATGTTG-----GCTGACTGTCTGCCACCACTGACCGG 347  
Db 65 GlnCysLysLysHisAspGlyGlnValGluIleSerSerCysThrValAspArgAspThr 84  
QY 348 AAATCGAGTGCCAAATAGGTCTTTAC-----TACTATGACCCCAAAATTTCCGGAATCATGC 404  
Db 85 ValCysGlyCysArgLysAsnGlnTyrArgHisTyrAspHisGluAsnArgPheTyrCys 104  
QY 405 CGCCCATGTACCAAGTGTCCCAAGGAATCTCTGCTCCAGGAATGCAACTCCACAGCT 464  
Db 105 PheAsnCysSerLeuCysLeuAsnGly---ThrValHisLeuSerCysGlnGluLysGln 123

QY 465 AACACTGTGTGCAGT 479  
Db 124 AsnThrValCysThr 128  
RESULT 12  
US-10-218-102-423  
; Sequence 423, Application US/10218102  
; Publication No. US20030130827A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentzien, Joerg  
; APPLICANT: Dahiyat, Basil I.  
; APPLICANT: Desjarlais, John R.  
; APPLICANT: Hayes, Robert J.  
; APPLICANT: Vielmetter, Jost  
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries  
; FILE REFERENCE: A-67229-11/RET/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/10/218,102  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: US 09/927,790  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/311,545  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 60/324,899  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/351,937  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/352,103  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 432  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 423  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-218-102-423

Alignment Scores:  
Pred. No.: 1,25e-12 Length: 162  
Score: 213.50 Matches: 44  
Percent Similarity: 47.20% Conservative: 15  
Best Local Similarity: 35.20% Mismatches: 59  
Query Match: 7.90% Indels: 7  
DB: 9 Gaps: 4

US-09-855-266A-3 (1-1509) x US-10-218-102-423 (1-162)

QY 123 TGTCCCGATGGTGAATAC-----CAGTCTAATGATGTCGTGCAAGACCTGTGCC 173  
Db 5 CysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThrLysCysHis 24  
QY 174 TCAGGTACATTGTCAAGCGCCCTGCAAAATCCCATACTCAAGGACAAATGTGAGAAG 233  
Db 25 LysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGlu 44  
QY 234 TGTCAACCCAGGAACATTCACAGGGAAGATATGCGCTGCATGATGTTGAATTTGCTCC 293  
Db 45 CysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgAspCysLeuGlnCysSer 64  
QY 294 ACCTGTGATAAGACCAAGATATGTTG-----GCTGACTGTCTGCCACCACTGACCGG 347  
Db 65 GlnCysLysLysHisAspGlyGlnValGluIleSerSerCysThrValAspArgAspThr 84  
QY 348 AAATCGAGTGCCAAATAGGTCTTTAC-----TACTATGACCCCAAAATTTCCGGAATCATGC 404  
Db 85 ValCysGlyCysArgLysAsnGlnTyrArgHisTyrAspHisGluAsnArgPheTyrCys 104  
QY 405 CGCCCATGTACCAAGTGTCCCAAGGAATCTCTGCTCCAGGAATGCAACTCCACAGCT 464  
Db 105 PheAsnCysSerLeuCysLeuAsnGly---ThrValHisLeuSerCysGlnGluLysGln 123  
QY 465 AACACTGTGTGCAGT 479



; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 60/324,899  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/351,937  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/352,103  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 432  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 425  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-218-102-425

Alignment Scores:  
Pred. No.: 5,02e-12 Length: 162  
Score: 207.50 Matches: 43  
Percent Similarity: 48.00% Conservative: 17  
Best Local Similarity: 34.40% Mismatches: 58  
Query Match: 7.67% Indels: 7  
DB: 16 Gaps: 4

US-09-855-266A-3 (1-1509) x US-10-218-102-425 (1-162)

QY	123	TGTCGGATGGTGAATAC-----CAGTCTAATGATGCTGTGTGCAAGACCTGTCCC	173
DB	5	CysProGlnGlyLysTyrLeHisProGlnAsnSerIleCysCysThrLysCysHis	24
QY	174	TCAGGTACATTTGTCAAGGCGCCTGCAAAATCCCATCTACTCAAGGACAAATGTGAGAAG	233
DB	25	LysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGlu	44
QY	234	TGTCACCCAGGAACATTCACAGGAAAGTAATGGCTGCATGATGTGAACCTTGCTCC	293
DB	45	CysGluSerGlySerPheThrAlaSerGluAsnTrpLeuArgArgCysLeuLeuCysSer	64
QY	294	ACCTGTGATAAGACCAACAGATATGGTG-----GCTGACTGTCTGCCACCAGTGACCGG	347
DB	65	LysCysArgLysGluGluGlyGlnValGluIleSerSerCysThrValAspArgAspThr	84
QY	348	AAATGCGAGTGCCTTAC---TACTATGACCCCAAAATTCGGAATCATGC	404
DB	85	ValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeuPheGlnCys	104
QY	405	CGCCCATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACAGCT	464
DB	105	PheAsnCysSerLeuCysLeuAsnGly---ThrValHisLeuSerCysGlnGluLysGln	123
QY	465	AACACTGTGTGCAGT	479
DB	124	AsnThrValCysThr	128

Search completed: August 20, 2003, 13:54:15  
Job time : 71 secs